

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 09:54:28 ; Search time 75 Seconds  
(without alignments)  
1861.955 Million cell updates/sec

Title: US-10-031-241-35  
Perfect score: 5457  
Sequence: 1 TRIKEMPQKTFGELKNLPL.....RLWLQQLERKGRYKDVWAG 1048

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: A.Geneseq.101002.\*  
2: /SID2/gcgdata/geneseq/genesep-emb1/AA1980.DAT:\*  
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24: /SID2/gcgdata/geneseq/genesep-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5457	100.0	1048	22	AA1980.DAT
2	5457	100.0	1048	22	AA1981.DAT
3	5457	100.0	1048	22	AA1982.DAT
4	5457	100.0	1048	22	AA1983.DAT
5	5457	100.0	1048	22	AA1984.DAT
6	5457	100.0	1048	22	AA1985.DAT
7	5457	100.0	1048	22	AA1986.DAT
8	5457	100.0	1048	22	AA1987.DAT
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10	5457	100.0	1048	22	AA1989.DAT
11	5457	100.0	1048	22	AA1990.DAT
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21	5457	100.0	1048	22	AA2000.DAT
22	5457	100.0	1048	22	AA2001.DAT
23	5457	100.0	1048	22	AA2002.DAT

Result No.	Score	Query Match	Length	ID	Description
1	5457	100.0	1048	22	AA1980.DAT
2	5457	100.0	1048	22	AA1981.DAT
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7	5457	100.0	1048	22	AA1986.DAT
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10	5457	100.0	1048	22	AA1989.DAT
11	5457	100.0	1048	22	AA1990.DAT
12	5457	100.0	1048	22	AA1991.DAT
13	5457	100.0	1048	22	AA1992.DAT
14	5457	100.0	1048	22	AA1993.DAT
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16	5457	100.0	1048	22	AA1995.DAT
17	5457	100.0	1048	22	AA1996.DAT
18	5457	100.0	1048	22	AA1997.DAT
19	5457	100.0	1048	22	AA1998.DAT
20	5457	100.0	1048	22	AA1999.DAT
21	5457	100.0	1048	22	AA2000.DAT
22	5457	100.0	1048	22	AA2001.DAT
23	5457	100.0	1048	22	AA2002.DAT

#### ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description
1	5457	100.0	1048	22	AA1980.DAT
2	5457	100.0	1048	22	AA1981.DAT
3	5457	100.0	1048	22	AA1982.DAT
4	5457	100.0	1048	22	AA1983.DAT
5	5457	100.0	1048	22	AA1984.DAT
6	5457	100.0	1048	22	AA1985.DAT
7	5457	100.0	1048	22	AA1986.DAT
8	5457	100.0	1048	22	AA1987.DAT
9	5457	100.0	1048	22	AA1988.DAT
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20	5457	100.0	1048	22	AA1999.DAT
21	5457	100.0	1048	22	AA2000.DAT
22	5457	100.0	1048	22	AA2001.DAT
23	5457	100.0	1048	22	AA2002.DAT

PT especially for converting indole to indigo, has wide substrate range -  
 XX Claim 3; Page 35-39; 54pp; German.  
 XX The present sequence represents a cytochrome P450 monooxygenase. The  
 CC specification describes a modified cytochrome P450 monooxygenase which  
 CC can oxidize at least one of the following types of substrates:  
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics  
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or  
 CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or  
 CC optionally substituted cycloalkanes or cycloalkenes. The modified  
 CC cytochrome P450 monooxygenase are specifically used to oxidize indole  
 CC to indigo and indorubicin. However, they may be used to oxidise many  
 CC other substrates.  
 XX  
 SQ Sequence 1048 AA;  
 Query Match 100.0%; Score 5457; DB 22; Length 1048;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTEGELKNPLNTDKPVQALMKIADLGIEFKFEAPGRVTRILSSORLIKE 60  
 DB 1 TIKEMPOKTEGELKNPLNTDKPVQALMKIADLGIEFKFEAPGRVTRILSSORLIKE 60  
 QY ACDESRFDKXLSQALKFVRDPAGDGLFTSWTHEKNMKKANHILPSFSQAMKGYHAMV 120  
 DB ACDESRFDKXLSQALKFVRDPAGDGLFTSWTHEKNMKKANHILPSFSQAMKGYHAMV 120  
 QY 61 ACDESRFDKXLSQALKFVRDPAGDGLFTSWTHEKNMKKANHILPSFSQAMKGYHAMV 120  
 DB 61 ACDESRFDKXLSQALKFVRDPAGDGLFTSWTHEKNMKKANHILPSFSQAMKGYHAMV 120  
 QY 121 DIAVOLVOKMERLNADEHIEVEDEMTRIITDTIGCGENYRPNSEFYRDPHPITTSVRA 180  
 DB 121 DIAVOLVOKMERLNADEHIEVEDEMTRIITDTIGCGENYRPNSEFYRDPHPITTSVRA 180  
 QY 121 DIAVOLVOKMERLNADEHIEVEDEMTRIITDTIGCGENYRPNSEFYRDPHPITTSVRA 180  
 DB 121 DIAVOLVOKMERLNADEHIEVEDEMTRIITDTIGCGENYRPNSEFYRDPHPITTSVRA 180  
 QY 181 LDEAMNKLOGRANPPDPAYDENKROFOEDIKYMNLDVDTIDRKASGSDLLTHMNG 240  
 DB 181 LDEAMNKLOGRANPPDPAYDENKROFOEDIKYMNLDVDTIDRKASGSDLLTHMNG 240  
 QY 241 KDPETGEPLDENIRYQIITFLIGHETTSGLSFALYLVKNPHVLQKAAEAAVLYD 300  
 DB 241 KDPETGEPLDENIRYQIITFLIGHETTSGLSFALYLVKNPHVLQKAAEAAVLYD 300  
 QY 301 PVPSYKQVKQLKYVGMVINEALRLMPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLLPOL 360  
 DB 301 PVPSYKQVKQLKYVGMVINEALRLMPTAPAFSLYAKEDTVLGGEYPLEKGDMLVLLPOL 360  
 QY 361 HRDKTIMGDDVEERPERFENPSAIPQHAFFKPFNGGQACIGQOFALHEATVLVGMMLKH 420  
 DB 361 HRDKTIMGDDVEERPERFENPSAIPQHAFFKPFNGGQACIGQOFALHEATVLVGMMLKH 420  
 QY 421 FDFEDHTNYELDIKETLTLLKPEGFVVKAKSKKIPLGIGIPSESTEOSAKVKKAKENAHNT 480  
 DB 421 FDFEDHTNYELDIKETLTLLKPEGFVVKAKSKKIPLGIGIPSESTEOSAKVKKAKENAHNT 480  
 QY 481 PLVLVYGSNMGTAAGTADLADIANVSKGPAQVATLDSHAGNLPREGAVLITVASYNGHP 540  
 DB 481 PLVLVYGSNMGTAAGTADLADIANVSKGPAQVATLDSHAGNLPREGAVLITVASYNGHP 540  
 QY 541 PDNAKOPVDMYDOASADVEKGVRSVFGCGDKNNAATTQKPAFDEFLAKGAEINADR 600  
 DB 541 PDNAKOPVDMYDOASADVEKGVRSVFGCGDKNNAATTQKPAFDEFLAKGAEINADR 600  
 QY 601 GEADASDDFEGTVEYREHMHMSDVAAAYFNLDIENSEDNKSTLSIQFVDSAADMLPAKHG 660  
 DB 601 GEADASDDFEGTVEYREHMHMSDVAAAYFNLDIENSEDNKSTLSIQFVDSAADMLPAKHG 660  
 QY 661 AFSTNNVASKELQOPGASRSTRHLEIEPKASAYOEGDHLGVIPRNYEGIVNRYTARFGL 720  
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 QY 721 DASOQIRLEAEBEKLAHLPLAKTVSVEELLQYVELQODVTRTQLRAMAAKTVCPPHKVEL 780  
 DB 721 DASOQIRLEAEBEKLAHLPLAKTVSVEELLQYVELQODVTRTQLRAMAAKTVCPPHKVEL 780

QY 781 EALLKQAYKEQVLAKRLTMLLEKYPACEMKRFSEFIALPSIRRYVSISSPRVDEK 840  
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 QY 841 QASITTSVVGEMWSGYGEYKGIASNYLAELQSGDITTCITSTPQSEFTLPKPBETLLM 900  
 DB 841 QASITTSVVGEMWSGYGEYKGIASNYLAELQSGDITTCITSTPQSEFTLPKPBETLLM 900  
 QY 901 VGPQGTGAPPRGFVQARKKQKEQOSIGEAHLTFGCRSPBEDLYOBELENAQSEGITL 960  
 DB 901 VGPQGTGAPPRGFVQARKKQKEQOSIGEAHLTFGCRSPBEDLYOBELENAQSEGITL 960  
 QY 961 HTAFSRMNPQKTYVGHVMEQDKKULIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 DB 961 HTAFSRMNPQKTYVGHVMEQDKKULIELLDQGAHFYICGDSQMAPAVEATLMKSYADV 1020  
 QY 1021 HOVSEADARLMLQOLEKGRYADWAG 1048  
 DB 1021 HOVSEADARLMLQOLEKGRYADWAG 1048

RESULT 2  
 AAB46855  
 ID AAB46855 standard; Protein; 1048 AA.  
 XX AAB46855;  
 AC AAB46855;  
 XX AAB46855;  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE B. megaterium cytochrome P450 monooxygenase BM-3 protein.  
 XX Cytochrome P450 monooxygenase; BM-3; electron donor system; bioreactor;  
 XX electron transfer; hydroxylatable fatty acid; fatty acid-monooxygenase.  
 OS Bacillus megaterium.  
 XX  
 PN W020107573-A1.  
 XX  
 PD 01-FEB-2001.  
 XX  
 PR 27-JUL-2000; 2000MO-EP07251.  
 XX  
 PR 27-JUL-1999; 99DE-1035115.  
 XX  
 PR 10-MAR-2000; 2000DE-1011723.  
 XX  
 PA (BADI ) BASF AG.  
 XX  
 PI Hauser B, Schmid RD, Schwaneberg U;  
 XX  
 DR WPI; 2001-159709/16.  
 XX  
 DR N-PSDB; AAF26268.  
 XX  
 PT Novel electron donor system useful for the production of  
 PT omega-hydroxylated fatty acids comprises an inorganic electron sink and  
 PT a mediator which enables the electron transfer -  
 XX  
 PS Claim 13b; Page 83-86; 94pp; German.  
 XX  
 CC This invention describes a novel electron donor system (M1) that  
 CC transfers electrons to an enzyme with redox properties comprising an  
 CC inorganic, not electrode-bound, electron sink and a mediator which enable  
 CC the electron transfer. The invention also describes (1) transferring (M2)  
 CC oxygen to a hydrocarbon containing hydrogen donor molecule, where the  
 CC hydrogen donor molecule is in a reaction medium comprising the oxygen  
 CC transferring enzyme and (M1) in the presence of oxygen and incubating  
 CC under suitable reaction conditions; (2) the enzymatic production (M3) of  
 CC terminally or subterminally hydroxylated (position omega-1 to omega-4)  
 CC fatty acids comprising: (1) mixing a hydroxylatable fatty acid or fatty  
 CC acid derivative in the presence of (M1) and cytochrome P450  
 CC monooxygenase; and (1i) isolating the hydroxylated product; (3) a  
 CC bioreactor useful for the production of omega-hydroxylated fatty acids as  
 CC described in (2); and (4) detecting (M4) fatty acid-monooxygenases  
 CC comprising: (1) contacting the analyte with a omega-hydroxylatable fatty

CC acid or a derivative comprising a terminal chromophore or fluorescent  
 CC label in (M); and (ii) qualitatively or quantitatively detecting the  
 CC signal. The invention is useful for the production of omega-hydroxylated  
 CC fatty acids and the detection of fatty acid monooxygenases. The  
 CC invention provides an alternative electron donor system of enzymes with  
 CC redox properties that is cheaper and more efficient, where the enzyme  
 CC comprises cytochrome 450.

XX Sequence 1048 AA;

Query Match 100.0%; Score 5457; DB 22; Length 1048;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 TIKEMPOPTFGELKPLPLNTDTPVQALMKIADDELGEIKFEAPGRVTRYSORLIKE 60  
 QY 61 ACDESREDKSLQALKFVRDPAGDGLFTSWTHEKNMKKANILLPSFSQAMKGYHAMV 120  
 DB 61 ACDESREDKSLQALKFVRDPAGDGLFTSWTHEKNMKKANILLPSFSQAMKGYHAMV 120  
 QY 121 DIAVOLVOKKERLNADHIEVPEDMTRLTDITGLCGFNTRFNSFYRDQHPPTTSWVRA 180  
 DB 121 DIAVOLVOKKERLNADHIEVPEDMTRLTDITGLCGFNTRFNSFYRDQHPPTTSWVRA 180  
 QY 181 LDEAMNKLQANPDPPAYDENKQFOEDIKYMDLVKIIADRAKASEGSDLLTHMLNG 240  
 DB 181 LDEAMNKLQANPDPPAYDENKQFOEDIKYMDLVKIIADRAKASEGSDLLTHMLNG 240  
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 DB 241 KDBETGEPLDENIRYOITFLIAGHETSGLSFALYFLVKNPHVLQKAEEARVLVD 300  
 QY 301 PVPSYKQVKQLKYVGWMLNEMALRMPAPASLYAKEDTVLGGRYPLEKGDMLVLLPOL 360  
 DB 301 PVPSYKQVKQLKYVGWMLNEMALRMPAPASLYAKEDTVLGGRYPLEKGDMLVLLPOL 360  
 QY 361 HRDKTIWGDVVEEPRFENPSAIPQAPKPFNGORACIGQGFALHEATLVGMMLKH 420  
 DB 361 HRDKTIWGDVVEEPRFENPSAIPQAPKPFNGORACIGQGFALHEATLVGMMLKH 420  
 QY 421 FDFEDHTNVELDIKETLLKPEGFVVAKSKKIPLGGI PSBSTEQSAKKVKKAKENAMHT 480  
 DB 421 FDFEDHTNVELDIKETLLKPEGFVVAKSKKIPLGGI PSBSTEQSAKKVKKAKENAMHT 480  
 QY 481 PLVLVYGSNNGTAEGRADLADIAMSGFAPOVATLDSHAGNLPREBGAVLIVTASYNGHP 540  
 DB 481 PLVLVYGSNNGTAEGRADLADIAMSGFAPOVATLDSHAGNLPREBGAVLIVTASYNGHP 540  
 QY 541 PDNAKOPVMDLDOASAEVGVRSVFGCGDKXMAATTYQKVPAPAFIDETLAKGAMENADR 600  
 DB 541 PDNAKOPVMDLDOASAEVGVRSVFGCGDKXMAATTYQKVPAPAFIDETLAKGAMENADR 600  
 QY 601 GEADASDPEFGTYEEMREHMSDVAAFNLDIENSEDNKSTLSQFVDSADNPLAMKMG 660  
 DB 601 GEADASDPEFGTYEEMREHMSDVAAFNLDIENSEDNKSTLSQFVDSADNPLAMKMG 660  
 QY 661 AESTNNVASELQOPGASARSTRHLEILPREASVOEGDHLCVTPRYEGIVNRTAFRGL 720  
 DB 661 AESTNNVASELQOPGASARSTRHLEILPREASVOEGDHLCVTPRYEGIVNRTAFRGL 720  
 QY 721 DASQOIRLEAEEELALPLAKTVSVELLYOYVELQDPVTRTOQRAMAATKVCPPHVEL 780  
 DB 721 DASQOIRLEAEEELALPLAKTVSVELLYOYVELQDPVTRTOQRAMAATKVCPPHVEL 780  
 QY 781 EALLEKQAYKEOVLAKLTLMLLELKYTPACEMKSEFIALPSIRPYISSSPRYDEK 840  
 DB 781 EALLEKQAYKEOVLAKLTLMLLELKYTPACEMKSEFIALPSIRPYISSSPRYDEK 840  
 QY 841 QASITTVSVSGEAMSGYGEYKGIASNTYLAIEQEDTITTCFISTQSEFTLPKDPETPLIM 900  
 DB 841 QASITTVSVSGEAMSGYGEYKGIASNTYLAIEQEDTITTCFISTQSEFTLPKDPETPLIM 900

QY 901 VGGTGVAPFRGVQARKOLKEQGOSLGEAHLFYGCRSPHEDYLYOBELEMAQSEGITTL 960  
 DB 901 VGGTGVAPFRGVQARKOLKEQGOSLGEAHLFYGCRSPHEDYLYOBELEMAQSEGITTL 960  
 QY 961 HTAFSMPNPQPKTYOVHNEBQDKKLIILLDQAHFYICGDSQMAPVAEATLMKSYADV 1020  
 DB 961 HTAFSMPNPQPKTYOVHNEBQDKKLIILLDQAHFYICGDSQMAPVAEATLMKSYADV 1020  
 QY 1021 HOVSADARLMLQOLEKGRYAKDVWAG 1048  
 DB 1021 HOVSADARLMLQOLEKGRYAKDVWAG 1048

# RESULT 3

AAAB46856  
 ID AAAB46856 standard; Protein; 1048 AA.  
 XX  
 AC AAAB46856;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE B. megaterium cytochrome P450 monooxygenase Bm-3 protein.  
 XX  
 KM Cytochrome P450 monooxygenase; Bm-3; site-specific mutagenesis;  
 XX aliphatic carboxylic acid hydroxylation; fatty acid.  
 OS Bacillus megaterium.  
 XX  
 FN W0200107574-A2.  
 PN  
 PD 01-FEB-2001.  
 XX  
 PF 27-JUL-2000; 2000MO-EP07252.  
 XX  
 PR 27-JUL-1999; 99DE-1035115.  
 XX  
 PR 10-MAR-2000; 2000DE-1011723.  
 XX  
 PA (BADI ) BASF AG.  
 XX  
 PI Häner B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;  
 PT Li Q;  
 XX  
 DR WPI; 2001-159710/16.  
 XX  
 DR N-PSDB; AAF26324.  
 XX  
 PT New modified cytochrome P450 mono-oxygenase, useful for producing  
 PT hydroxylated aliphatic carboxylic acids and derivatives, has altered  
 PT substrate specificity -  
 XX  
 PS Claim 3; Page 41-45; 49pp; German.  
 XX  
 CC This invention describes a novel modified cytochrome P450 (I) having, as  
 CC a result of site-specific mutagenesis of its substrate-binding domain,  
 CC an altered substrate profile, relative to the wild-type, when used for  
 CC terminal and/or subterminal enzymatic hydroxylation of aliphatic  
 CC carboxylic acids. The invention also describes (1) nucleic acid (II)  
 CC encoding (I), and its complement; (2) expression cassette (EC) containing  
 CC (II) and control elements; (3) a vector containing at least one EC; (4)  
 CC recombinant microorganisms transformed with at least one vector of (3);  
 CC and (5) enzymatic production of terminally and/or subterminally  
 CC hydroxylated aliphatic carboxylic acids (A) using the microorganisms of  
 CC (4), or isolated (I). (I), and recombinant cells that express them, are  
 CC used to produce hydroxylated aliphatic carboxylic acids or their  
 CC derivatives (esters and amides). (I) have altered substrate specificity,  
 CC especially for hydroxylation of 8-12C fatty acids at the omega-1, -2  
 CC and/or -3 positions, and may also have increased reactivity and/or  
 CC regioselectivity.  
 XX  
 SO Sequence 1048 AA;  
 Query Match 100.0%; Score 5457; DB 22; Length 1048;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 TIKEMPOKTEGELKNLPLINTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE 60
Db 1 TIKEMPOKTEGELKNLPLINTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE 60
QY 61 ACDESREDFKNLSQALKFVRDPADGDLFTSWTHEKNWKKAHNILLPSFSQAMKGYHAMMV 120
Db 61 ACDESREDFKNLSQALKFVRDPADGDLFTSWTHEKNWKKAHNILLPSFSQAMKGYHAMMV 120
QY 121 DIAVOLVOKMERLNADENIEVPEDMTRLLDTTGLCGFNFRFNSYRQPHPTTSMWRA 180
Db 121 DIAVOLVOKMERLNADENIEVPEDMTRLLDTTGLCGFNFRFNSYRQPHPTTSMWRA 180
QY 121 DIAVOLVOKMERLNADENIEVPEDMTRLLDTTGLCGFNFRFNSYRQPHPTTSMWRA 180
Db 121 DIAVOLVOKMERLNADENIEVPEDMTRLLDTTGLCGFNFRFNSYRQPHPTTSMWRA 180
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Db 181 LDEAMNKLQRANPPDPAYDENKROFOEDIKYMNLDVDCIINDRASGSGSDLLTHMLNG 240
QY 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLSPALYLVKNPHVLQKAEBAARVLVD 300
Db 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLSPALYLVKNPHVLQKAEBAARVLVD 300
QY 301 PVPSYKQVKOLKYVGMVINEALRLMPTAPASLYAKEPTVYGGEPLEKGDMLVLLPOL 360
Db 301 PVPSYKQVKOLKYVGMVINEALRLMPTAPASLYAKEPTVYGGEPLEKGDMLVLLPOL 360
QY 361 HRDKTIWGDDVEEERPERFENPSAIPOHAFKPFNGORACIGQOPALHEATLVYGMMLKH 420
Db 361 HRDKTIWGDDVEEERPERFENPSAIPOHAFKPFNGORACIGQOPALHEATLVYGMMLKH 420
QY 421 FDFEDHTNYELDIKETTLTKPEGFVYKAKSKKIPLGIGIPSPSTEQSAKVKAKKANAHT 480
Db 421 FDFEDHTNYELDIKETTLTKPEGFVYKAKSKKIPLGIGIPSPSTEQSAKVKAKKANAHT 480
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Db 481 PLVLVGSNMGTAAGTARDLADLAMSKGAPOVATLDSHAENLPREGVLLVTLASYNCHP 540
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Db 541 PDNAKQFDMLDQASADEVKGVRSVFCGDKMNAATTQKPAFIDETLAKAGENIADR 600
QY 601 GEADASDDFEGTYEEMREHMSDVAAVFNLDIENSEDNKSTLSIQFVDSAADMLAKMKG 660
Db 601 GEADASDDFEGTYEEMREHMSDVAAVFNLDIENSEDNKSTLSIQFVDSAADMLAKMKG 660
QY 661 AFSTNVASKELOQPGSARSTRHLEIELPKASVOEGDHLGVIIRNVEGINRTARFGL 720
Db 661 AFSTNVASKELOQPGSARSTRHLEIELPKASVOEGDHLGVIIRNVEGINRTARFGL 720
QY 721 DASQOIRLEAESEKLAHLPLAKTVSVEBLQYVELODPVTRTQRLAMAAKVCCEPHKVEL 780
Db 721 DASQOIRLEAESEKLAHLPLAKTVSVEBLQYVELODPVTRTQRLAMAAKVCCEPHKVEL 780
QY 781 EALLEKQAYKQVIAKRLTMELELEKYPACEMKCFSEFIALIPISIRPRYSSISSPRVDEK 840
Db 781 EALLEKQAYKQVIAKRLTMELELEKYPACEMKCFSEFIALIPISIRPRYSSISSPRVDEK 840
QY 841 QASITVSVGEAMSGVEYKGIASNYIAELOEDDTTCFSTQSESTLTKDDETPILIM 900
Db 841 QASITVSVGEAMSGVEYKGIASNYIAELOEDDTTCFSTQSESTLTKDDETPILIM 900
QY 901 VGPSTGVAPFRGFVQARQKOLKEGOSLGEAHLFGCGRSPHEDVYQOELLENASQEGITTL 960
Db 901 VGPSTGVAPFRGFVQARQKOLKEGOSLGEAHLFGCGRSPHEDVYQOELLENASQEGITTL 960
QY 961 HTAFSRMNPQRTYVOHVMEODGKLLIELDQGAHFYICGDGSGQAPAVEATLTKSYADV 1020
Db 961 HTAFSRMNPQRTYVOHVMEODGKLLIELDQGAHFYICGDGSGQAPAVEATLTKSYADV 1020
QY 1021 HOVEADARLMLQOLEEKGRYAKDVWAG 1048
Db 1021 HOVEADARLMLQOLEEKGRYAKDVWAG 1048

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RESULT 4
AA93566
ID AA93566 standard; Protein; 1049 AA.
AC AA93566;
DT 25-SEP-2000 (first entry)
DE Amino acid sequence of the P450-BM3 sequence.
KM Terpene; cycloalkene; haem-containing enzyme; mutant; oxidation;
infection; P450-BM3.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 303
FT /note= "Val encoded by GCT"
FT Misc-difference 471
FT /note= "Val encoded by GCA"
XX
XX W0200031273-A2.
XX
XX 02-JUN-2000.
XX
XX 19-NOV-1999; 99MO-GB03873.
XX
XX 19-NOV-1998; 98GB-0025421.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Wong LL, Bell SG, Carmichael AB;
XX
XX WPI; 2000-451679/39.
XX
XX N-PSDB; AAA46648.
XX
XX Process for oxidizing acyclic or cyclic terpenes, cycloalkenes, or
XX derivatives for preventing or treating infection in human or animal
XX body comprises mutant haem-containing enzyme which has substitution of
XX amino acid in the active site -
XX
XX Disclosure; Page 51-53; 63pp; English.
XX
XX The specification describes a process for oxidizing an acyclic or
XX cyclic terpene, a cycloalkene, or a derivative. The process comprises
XX oxidizing the compound with a mutant haem-containing enzyme which
XX comprises a substitution of an amino acid in the active site by an
XX amino acid with a less polar side-chain. The process is useful for
XX oxidizing an acyclic or cyclic terpene, a cycloalkene, or their
XX derivatives. The process is also useful for producing an oxidation
XX product useful for preventing or treating infection in a human or
XX animal body. The present sequence represents the amino acid sequence of
XX the P450-BM3 sequence. The protein is used to construct enzymes
XX for use in the process of the invention.
XX
XX Sequence 1049 AA:
QY Query Match 100.0%; Score 5457; DB 21; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TIKEMPOKTEGELKNLPLINTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE 60
Db 2 TIKEMPOKTEGELKNLPLINTDKPVQALMKIADLGEIFKFEAPGRVTRYLSSORLIKE 61
QY 61 ACDESREDFKNLSQALKFVRDPADGDLFTSWTHEKNWKKAHNILLPSFSQAMKGYHAMMV 120
Db 62 ACDESREDFKNLSQALKFVRDPADGDLFTSWTHEKNWKKAHNILLPSFSQAMKGYHAMMV 121
QY 121 DIAVOLVOKMERLNADENIEVPEDMTRLLDTTGLCGFNFRFNSYRQPHPTTSMWRA 180
Db 121 DIAVOLVOKMERLNADENIEVPEDMTRLLDTTGLCGFNFRFNSYRQPHPTTSMWRA 180

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Db      122 DIAVOLVOKMERLNADENHIEVPEDMTRLTLDTIGLCGFNYRNFNSFYRDQPHFITSMVRA 181
Qy      181 LDEAMNKLORANPDPAVDENKROFOEDIKVMNDLVOKIIADRKASGEOSDILLTHMLNG 240
Db      182 LDEAMNKLORANPDPAVDENKROFOEDIKVMNDLVOKIIADRKASGEOSDILLTHMLNG 241
Qy      241 KDBETGEPLDENIRYOIITFLIAGHETTSGLSFLALYLVKNPHVLOKAAEBAARLVLD 300
Db      242 KDBETGEPLDENIRYOIITFLIAGHETTSGLSFLALYLVKNPHVLOKAAEBAARLVLD 301
Qy      301 PVPSTYKOVOLKTVGVNLEALRLMPTAPAFSLYAKEDTVLGGEYPLEKDELMVLI.POL 360
Db      302 PVPSTYKOVOLKTVGVNLEALRLMPTAPAFSLYAKEDTVLGGEYPLEKDELMVLI.POL 361
Qy      361 HRDKTIWGDVEEERPERFENPSAIPQAHFKPFGNGORACIGQGFALHEATVLVGMMLKH 420
Db      362 HRDKTIWGDVEEERPERFENPSAIPQAHFKPFGNGORACIGQGFALHEATVLVGMMLKH 421
Qy      421 FDEEDHTNVELDIKETITLTKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVKKAEANAHT 480
Db      422 FDEEDHTNVELDIKETITLTKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVKKAEANAHT 481
Qy      481 PLLVLVYGSNMGTABGTARDIADIAKSGFAPQVATLDSHAGNLPRBGAVLIVTASYNGHP 540
Db      482 PLLVLVYGSNMGTABGTARDIADIAKSGFAPQVATLDSHAGNLPRBGAVLIVTASYNGHP 541
Qy      541 PDNAKQFVMDLDOASADEVGVSVSGCGDKMMAATYQVAPFIDETLAKAENADR 600
Db      542 PDNAKQFVMDLDOASADEVGVSVSGCGDKMMAATYQVAPFIDETLAKAENADR 601
Qy      601 GEADASDDEFGTYEEMREHMSDVAAAFNLDIENSEDNKSTLSLOFDSAADPLAMMG 660
Db      602 GEADASDDEFGTYEEMREHMSDVAAAFNLDIENSEDNKSTLSLOFDSAADPLAMMG 661
Qy      661 AESTNVASAKELQOPGSAKSTRLIEFLPKASVYQSGDLGVIPRNYEGIVNRYTARFGL 720
Db      662 AESTNVASAKELQOPGSAKSTRLIEFLPKASVYQSGDLGVIPRNYEGIVNRYTARFGL 721
Qy      721 DASQOIRLEAEERKLALPLAKTVSVLELOVVELLODPVTRTORAMAATVCPHVEL 780
Db      722 DASQOIRLEAEERKLALPLAKTVSVLELOVVELLODPVTRTORAMAATVCPHVEL 781
Qy      781 EALLEKQAVKEOYLAKLITMLELEKYRACEMKFSERIALLPISRPYVSISSPRVDEK 840
Db      782 EALLEKQAVKEOYLAKLITMLELEKYRACEMKFSERIALLPISRPYVSISSPRVDEK 841
Qy      841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPOSFTLPKDETPLM 900
Db      842 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPOSFTLPKDETPLM 901
Qy      901 VGGGTGVAAPRGVQARQKQKEOGOSIGEAHLVFGCSRHEDTVLYOBELNASEGIIITL 960
Db      902 VGGGTGVAAPRGVQARQKQKEOGOSIGEAHLVFGCSRHEDTVLYOBELNASEGIIITL 961
Qy      961 HTAFSEMPNPKTYVQHVMEQDGKLELIDOGAHFICDGSQMAVAEATLMKSTADV 1020
Db      962 HTAFSEMPNPKTYVQHVMEQDGKLELIDOGAHFICDGSQMAVAEATLMKSTADV 1021
Qy      1021 HOVSEADARIMLQOLEEKGRYAKDVWAG 1048
Db      1022 HOVSEADARIMLQOLEEKGRYAKDVWAG 1049

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RESULT 5  
AAB31882  
ID AAB31882 standard; Protein; 1049 AA.  
XX  
XX AAB31882;  
AC  
XX  
XX  
DT 15-MAY-2001 (first entry)  
DE  
XX

Amino acid sequence of a Bacillus P450 monooxygenase protein.

```

KM      Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.
XX
OS      Bacillus megaterium.
XX
PN      W0200107630-A1.
XX
PD      01-FEB-2001.
XX
PF      27-JUL-2000; 2000MO-EP07253.
XX
PR      27-JUL-1999; 99DE-1035115.
PR      18-NOV-1999; 99DE-1055605.
PR      22-MAR-2000; 2000DE-1014085.
XX
PA      (BADI ) BASF AG.
XX
PI      Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;
PI      Ia Q;
DR      WPI; 2001-182800/18.
XX
PT      Cytochrome P450 monooxygenase for oxidizing organic compounds, useful
PT      especially for converting indole to indigo, has wide substrate range
XX
PS      Disclosure; Page 41-44; 54pp; German.
XX
CC      The present sequence represents a cytochrome P450 monooxygenase. The
CC      specification describes a modified cytochrome P450 monooxygenase which
CC      can oxidize at least one of the following types of substrates:
CC      optionally substituted mono- or poly-cyclic aromatic heterocyclics
CC      containing nitrogen, sulphur or oxygen; optionally substituted mono- or
CC      poly-cyclic aromatics; linear or branched alkanes or alkenes; or
CC      optionally substituted cycloalkanes or cycloalkenes. The modified
CC      cytochrome P450 monooxygenase are specifically used to oxidize indole
CC      to indigo and indorubicin. However, they may be used to oxidise many
CC      other substrates.
XX
SQ      Sequence 1049 AA;

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Query Match 100.0%; Score 5457; DB 22; Length 1049;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1048; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TIKEMPOPTFGELKULPLNTDQPVQALMKIADDELGEIFKFAPRVRYLSSORLIXE 60
Db      2 TIKEMPOPTFGELKULPLNTDQPVQALMKIADDELGEIFKFAPRVRYLSSORLIXE 61
Qy      61 ACDESERFDKLSQALKFVDFADGGLFTSWTHEKNKKKANHILPFSQOAMKGYHAMV 120
Db      62 ACDESERFDKLSQALKFVDFADGGLFTSWTHEKNKKKANHILPFSQOAMKGYHAMV 121
Qy      121 DIAVOLVOKMERLNADENHIEVPEDMTRLTLDTIGLCGFNYRNFNSFYRDQPHFITSMVRA 180
Db      122 DIAVOLVOKMERLNADENHIEVPEDMTRLTLDTIGLCGFNYRNFNSFYRDQPHFITSMVRA 181
Qy      181 LDEAMNKLORANPDPAVDENKROFOEDIKVMNDLVOKIIADRKASGEOSDILLTHMLNG 240
Db      182 LDEAMNKLORANPDPAVDENKROFOEDIKVMNDLVOKIIADRKASGEOSDILLTHMLNG 241
Qy      241 KDBETGEPLDENIRYOIITFLIAGHETTSGLSFLALYLVKNPHVLOKAAEBAARLVLD 300
Db      242 KDBETGEPLDENIRYOIITFLIAGHETTSGLSFLALYLVKNPHVLOKAAEBAARLVLD 301
Qy      301 PVPSTYKOVOLKTVGVNLEALRLMPTAPAFSLYAKEDTVLGGEYPLEKDELMVLI.POL 360
Db      302 PVPSTYKOVOLKTVGVNLEALRLMPTAPAFSLYAKEDTVLGGEYPLEKDELMVLI.POL 361
Qy      361 HRDKTIWGDVEEERPERFENPSAIPQAHFKPFGNGORACIGQGFALHEATVLVGMMLKH 420
Db      362 HRDKTIWGDVEEERPERFENPSAIPQAHFKPFGNGORACIGQGFALHEATVLVGMMLKH 421
Qy      421 FDEEDHTNVELDIKETITLTKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVKKAEANAHT 480

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Db 422 FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGISPSTEQSAKAKKKAENAHNT 481
Qy 481 PLVLVYGSNMGTAGTARDLADLADIMSKGFAPOVALTLDSHAGNLPREGAVLIVTASVNGHP 540
Db 482 PLVLVYGSNMGTAGTARDLADLADIMSKGFAPOVALTLDSHAGNLPREGAVLIVTASVNGHP 541
Qy 541 PDNAKQFVDWLDQASADEVKGVRSVFGCGDKMATTYQKVPAPFIDETTLAKGAMENADR 600
Db 542 PDNAKQFVDWLDQASADEVKGVRSVFGCGDKMATTYQKVPAPFIDETTLAKGAMENADR 601
Qy 601 GEADASDDFEGTYEEMREHMSDVAAAYFNLDIENSSEDKSTLSIQFVDSAADMPLAKMHG 660
Db 602 GEADASDDFEGTYEEMREHMSDVAAAYFNLDIENSSEDKSTLSIQFVDSAADMPLAKMHG 661
Qy 661 AFSTNVASKELOPGASRSTRHLETELPEKASVOEGPHLGVTIRNVEGIVNRVTARFGL 720
Db 662 AFSTNVASKELOPGASRSTRHLETELPEKASVOEGPHLGVTIRNVEGIVNRVTARFGL 721
Qy 721 DASOQIRLEAEKEELAHPLAKTVSVEELLQYVELQDPVTRTQLRAMAKTVCPHKKVEL 780
Db 722 DASOQIRLEAEKEELAHPLAKTVSVEELLQYVELQDPVTRTQLRAMAKTVCPHKKVEL 781
Qy 781 EALLEKQAYKEQVLAQRITMLELLEKYPACMKCSEPTALLPSIRPRYSSISSPRVDEK 840
Db 782 EALLEKQAYKEQVLAQRITMLELLEKYPACMKCSEPTALLPSIRPRYSSISSPRVDEK 841
Qy 841 QASITVSVSGEAMSGVEYKGIASNYLAEOEGDTTCFSTQSEPTLPKDEPTPLIM 900
Db 842 QASITVSVSGEAMSGVEYKGIASNYLAEOEGDTTCFSTQSEPTLPKDEPTPLIM 901
Qy 901 VGPSTGVAFFRGFYQARKOLKEQOSLGEAHLYFGCRSPHEDYLYQBELNAQSGIITL 960
Db 902 VGPSTGVAFFRGFYQARKOLKEQOSLGEAHLYFGCRSPHEDYLYQBELNAQSGIITL 961
Qy 961 HTASRMPNOCKTYQVHMEODGKLLLELDQGAFFYCGSGSQMAPVEATLTKSYADV 1020
Db 962 HTASRMPNOCKTYQVHMEODGKLLLELDQGAFFYCGSGSQMAPVEATLTKSYADV 1021
Qy 1021 HOVEADARLWLOOLEEKGRYAKDVWAG 1048
Db 1022 HOVEADARLWLOOLEEKGRYAKDVWAG 1049

RESULT 6
AAB31979
ID AAB31979 standard; Protein; 1048 AA.
AC AAB31979;
XX
XX 15-MAY-2001 (first entry)
DT
XX
XX Amino acid sequence of a modified P450 monooxygenase protein.
DE
XX
XX Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.
KM
XX
XX Bacillus megaterium.
OS
XX
XX Key Location/Qualifiers
FT Misc-difference 87 /note= "wild type Phe changed to Val"
XX
XX MO200107630-A1.
XX
XX 01-FEB-2001.
XX
XX 27-JUL-2000; 2000MO-EP07253.
XX
XX 27-JUL-1999; 99DE-1035115.
XX
XX 18-NOV-1999; 99DE-105605.
XX
XX 22-MAR-2000; 2000DE-1014085.
XX
XX (BADT ) BASF AG.
XX

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PI Haver B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;
PI Li Q;
XX WPI; 2001-182800/18.
XX
XX Cytochrome P450 monooxygenase for oxidizing organic compounds, useful
XX especially for converting indole to indigo, has wide substrate range
XX
XX Claim 5; Page -; 54pp; German.
XX
XX The present sequence represents a modified cytochrome P450 monooxygenase.
XX The specification describes a modified cytochrome P450 monooxygenase
XX which can oxidize at least one of the following types of substrates:
XX optionally substituted mono- or poly-cyclic aromatic heterocyclics
XX optionally substituted nitro-, sulphur or oxygen; optionally substituted mono- or
XX poly-cyclic aromatics; linear or branched alkenes or alkenes; or
XX optionally substituted cycloalkanes or cycloalkenes. The modified
XX cytochrome P450 monooxygenase are specifically used to oxidize indole
XX to indigo and indorubicin. However, they may be used to oxidize many
XX other substrates.
XX note: this sequence does not appear in the specification; it was created
XX using information provided.
XX
XX Sequence 1048 AA;
SQ
Query Match 99.9%; Score 5450; DB 22; Length 1048;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1047; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TIKEMPQKTFEGELKNPLINTDKPVQALMKIADLCEIFKFAFGVTRYLSSQRLIKE 60
Db 1 TIKEMPQKTFEGELKNPLINTDKPVQALMKIADLCEIFKFAFGVTRYLSSQRLIKE 60
Qy 61 ACDESREFDKLSQALKVRDPAGGLFTSWTHEKMKKANILLPSQQAMGYHAMV 120
Db 61 ACDESREFDKLSQALKVRDPAGGLFTSWTHEKMKKANILLPSQQAMGYHAMV 120
Qy 121 DIAVOLQKMERLNADHEIEVPEDMTRLTDITGLCGFNRYFNSFYDQPHPTTSWRA 180
Db 121 DIAVOLQKMERLNADHEIEVPEDMTRLTDITGLCGFNRYFNSFYDQPHPTTSWRA 180
Qy 181 LDEAMNKLQRPANPDPAVDENKROFOEDIRYANDLVDKIADRKAQSGSDLLTHMLNG 240
Db 181 LDEAMNKLQRPANPDPAVDENKROFOEDIRYANDLVDKIADRKAQSGSDLLTHMLNG 240
Qy 241 KDPEGEPDDEMRVQIITFLAGHETTSGLSFALYFLVKMHPVQKAAEBAARVLVD 300
Db 241 KDPEGEPDDEMRVQIITFLAGHETTSGLSFALYFLVKMHPVQKAAEBAARVLVD 300
Qy 301 PVPSYKQVKOLKYGVNLNLRMLPTAPAFSLYAKEDTVLGEYPLEKGDMLVLIPOI 360
Db 301 PVPSYKQVKOLKYGVNLNLRMLPTAPAFSLYAKEDTVLGEYPLEKGDMLVLIPOI 360
Qy 361 HRDKTIWGDVEEFRPRFENPSAIPQAHKPRFGNGRACIGQGFALHEATLVGMWLK 420
Db 361 HRDKTIWGDVEEFRPRFENPSAIPQAHKPRFGNGRACIGQGFALHEATLVGMWLK 420
Qy 421 FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGISPSTEQSAKAKKKAENAHNT 480
Db 421 FDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGISPSTEQSAKAKKKAENAHNT 480
Qy 481 PLVLVYGSNMGTAGTARDLADLADIMSKGFAPOVALTLDSHAGNLPREGAVLIVTASVNGHP 540
Db 481 PLVLVYGSNMGTAGTARDLADLADIMSKGFAPOVALTLDSHAGNLPREGAVLIVTASVNGHP 540
Qy 541 PDNAKQFVDWLDQASADEVKGVRSVFGCGDKMATTYQKVPAPFIDETTLAKGAMENADR 600
Db 541 PDNAKQFVDWLDQASADEVKGVRSVFGCGDKMATTYQKVPAPFIDETTLAKGAMENADR 600
Qy 601 GEADASDDFEGTYEEMREHMSDVAAAYFNLDIENSSEDKSTLSIQFVDSAADMPLAKMHG 660
Db 601 GEADASDDFEGTYEEMREHMSDVAAAYFNLDIENSSEDKSTLSIQFVDSAADMPLAKMHG 660

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QY 661 AFSTNVASKELOQPSASRSTRLEIELPKEASYOEGDHLGVIPRNYEGIVNVTARFGL 720
DB 661 AFSTNVASKELOQPSASRSTRLEIELPKEASYOEGDHLGVIPRNYEGIVNVTARFGL 720
QY 721 DASQOIRLEAEERKLAHLPLAKTVSVBELLOQYVELDPPVTRTQIRAMAATVCPPHKVEL 780
DB 721 DASQOIRLEAEERKLAHLPLAKTVSVBELLOQYVELDPPVTRTQIRAMAATVCPPHKVEL 780
QY 781 EALLEQOAYKEQVLAKRLTLMLELEKYPACEMKFSFIALPISIRPRYISSSPRYDEK 840
DB 781 EALLEQOAYKEQVLAKRLTLMLELEKYPACEMKFSFIALPISIRPRYISSSPRYDEK 840
QY 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
DB 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
QY 901 VEGGTGVAAPRGVQARKOLKEGOSIGENHLYFGCSPHEDYLYOELENAOSEGITL 960
DB 901 VEGGTGVAAPRGVQARKOLKEGOSIGENHLYFGCSPHEDYLYOELENAOSEGITL 960
QY 961 HTAFSPMPNQKTYVOHVMEODGKLIELLDQAHFYTICGDSGOMAPAVEATLMKSYADV 1020
DB 961 HTAFSPMPNQKTYVOHVMEODGKLIELLDQAHFYTICGDSGOMAPAVEATLMKSYADV 1020
QY 1021 HQVSEADARLMLQOLEKEGRYAKDVWAG 1048
DB 1021 HQVSEADARLMLQOLEKEGRYAKDVWAG 1048

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RESULT 7  
AA72208  
AA72208 standard; Protein; 1049 AA.

XX AA72208;

XX 24-APR-2001 (first entry)

XX Bacillus megaterium monooxygenase enzyme homologue, P450BM-3.

XX Monooxygenase enzyme; P450BM-3 homologue; P450cam; oxidation;  
KM halogenated aromatic compound; electron transfer; putidaredoxin;  
KM putidaredoxin reductase; detoxification.

XX Bacillus megaterium.

XX MO200078973-A1.

XX 28-DEC-2000.

XX 19-JUN-2000; 2000MO-GB02379.

XX 18-JUN-1999; 99GB-0014373.

XX (ISIS-) ISIS INNOVATION LTD.

XX Wong LL, Jones JP;

XX WPI, 2001-071397/08.

XX N-PSDB; AAD02365.

XX New process for detoxifying environments contaminated with halo  
PT aromatic compounds comprises treating the affected area with a  
PT monooxygenase enzyme -

XX disclosuure; Page 32-39; 42pp; English.

XX The present invention relates to a process for enzymatically oxidising  
CC the halogenated aromatic compounds such as 1,2-dichlorobenzene,  
CC 1,2,4-trichlorobenzene, 3,3'-dichlorobiphenyl or 2,2',4,5,  
CC 5'-pentachlorobiphenyl. The process comprises treating the polluted  
CC environment with a monooxygenase enzyme. A monooxygenase enzyme, P450cam,  
CC and its physiological electron transfer partners, putidaredoxin and  
CC putidaredoxin reductase, are used to oxidise the halogenated aromatic

CC compounds. Also mutants of the monooxygenase enzyme with substitutions in  
CC the active site have enhanced oxidation activity. The process and the  
CC transgenic plant or animal which expresses the monooxygenase enzyme are  
CC used for detoxifying the environment polluted with the halo aromatic  
CC compounds. The present sequence is a Bacillus megaterium monooxygenase  
CC enzyme, P450BM-3, which is homologous to the monooxygenase  
CC enzyme, P450cam.

XX Sequence 1049 AA;

Query Match 99.9%; Score 5449; DB 22; Length 1049;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 TIKEMPQPTFGLKXUPLINTDKPQVQALMKLADELGEIFKFPAPRVTRYSORLIKE 60
DB 2 TIKEMPQPTFGLKXUPLINTDKPQVQALMKLADELGEIFKFPAPRVTRYSORLIKE 61
QY 61 ACDESRFDKXLSQALKFVDFADGGLFTSWTEKXKXKXNILLPSFSQAMKGYHAMV 120
DB 62 ACDESRFDKXLSQALKFVDFADGGLFTSWTEKXKXKXNILLPSFSQAMKGYHAMV 121
QY 121 DIAVLQVKMERLNADENIEVEPEDMTRLTLDITGLCGFYVRFPNSFYRDPHPPTISWVRA 180
DB 122 DIAVLQVKMERLNADENIEVEPEDMTRLTLDITGLCGFYVRFPNSFYRDPHPPTISWVRA 181
QY 181 LDEAMNKLORANDDDPAYDENKROFQEDIKVMNDLVDKIADKASGEOSDILLTMTLNG 240
DB 182 LDEAMNKLORANDDDPAYDENKROFQEDIKVMNDLVDKIADKASGEOSDILLTMTLNG 241
QY 241 KOPETGEPLDENIRYQIITFLIAGHETTSGLISFALYELVKNPHYLQKAEBAARVLD 300
DB 242 KOPETGEPLDENIRYQIITFLIAGHETTSGLISFALYELVKNPHYLQKAEBAARVLD 301
QY 301 PVPYSYQVQKQKTVGVNLNBAIRLMPFAPASLYAKEDTVLGSEYPLEKDELMVLI 360
DB 302 PVPYSYQVQKQKTVGVNLNBAIRLMPFAPASLYAKEDTVLGSEYPLEKDELMVLI 361
QY 361 HRDKTIWGDVVEFRERENPSAIPQAHFKPFGNORACIGQFPLHEATVILGMKLK 420
DB 362 HRDKTIWGDVVEFRERENPSAIPQAHFKPFGNORACIGQFPLHEATVILGMKLK 421
QY 421 FDFEDHTNVELDKETITLKEPGEFVVKAKSKKIPLGISPSSTEQSAKKVKKAEANAHT 480
DB 422 FDFEDHTNVELDKETITLKEPGEFVVKAKSKKIPLGISPSSTEQSAKKVKKAEANAHT 481
QY 481 PLIVLYGSMNGTAGTARDLADIAMSKGAPQVATLDISHAGNIPREGAVLITVASYNGHP 540
DB 482 PLIVLYGSMNGTAGTARDLADIAMSKGAPQVATLDISHAGNIPREGAVLITVASYNGHP 541
QY 541 PDNAKQFVMDLOASADDEVKGVYVFGCGDKRMATTYQKVPFIETTLAKGAENIADR 600
DB 542 PDNAKQFVMDLOASADDEVKGVYVFGCGDKRMATTYQKVPFIETTLAKGAENIADR 601
QY 601 GEADASDDFEGTYEERHEHMSDVAAYFNLDIENSDKSTLSIQVDSADAPLAKMHG 660
DB 602 GEADASDDFEGTYEERHEHMSDVAAYFNLDIENSDKSTLSIQVDSADAPLAKMHG 661
QY 661 AFSTNVASKELOQPSASRSTRLEIELPKEASYOEGDHLGVIPRNYEGIVNVTARFGL 720
DB 662 AFSTNVASKELOQPSASRSTRLEIELPKEASYOEGDHLGVIPRNYEGIVNVTARFGL 721
QY 721 DASQOIRLEAEERKLAHLPLAKTVSVBELLOQYVELDPPVTRTQIRAMAATVCPPHKVEL 780
DB 722 DASQOIRLEAEERKLAHLPLAKTVSVBELLOQYVELDPPVTRTQIRAMAATVCPPHKVEL 781
QY 781 EALLEQOAYKEQVLAKRLTLMLELEKYPACEMKFSFIALPISIRPRYISSSPRYDEK 840
DB 782 EALLEQOAYKEQVLAKRLTLMLELEKYPACEMKFSFIALPISIRPRYISSSPRYDEK 841
QY 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
DB 842 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901

```

QY 901 VGPCTGVAPRFGVQARKOLKEGOSLGEAHLFGCRSPHEDLYOBELENAOSEGITTL 960  
 DB 902 VGPCTGVAPRFGVQARKOLKEGOSLGEAHLFGCRSPHEDLYOBELENAOSEGITTL 961  
 QY 961 HTAFSRMPNPKTYVQHVMEQDGKLLIELDQGAHFYICGDSQMAVAEATLMKSYADV 1020  
 DB 962 HTAFSRMPNPKTYVQHVMEQDGKLLIELDQGAHFYICGDSQMAVAEATLMKSYADV 1021  
 QY 1021 HOVSADARLMLQOLEEKGRAKDVWAG 1048  
 DB 1022 HOVSADARLMLQOLEEKGRAKDVWAG 1049

RESULT 8  
 AAB31980  
 ID AAB31980 standard; Protein; 1048 AA.  
 AC AAB31980;  
 DT 15-MAY-2001 (first entry)  
 DE Amino acid sequence of a modified P450 monooxygenase protein.  
 KM Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.  
 OS Bacillus megaterium.  
 FH Key Location/Qualifiers  
 FT Misc-difference 87 /note= "wild type phe changed to Val"  
 FT Misc-difference 188 /note= "wild type Leu changed to Gln"  
 XX W0200107630-A1.  
 XX 01-FEB-2001.  
 PD 27-JUL-2000; 2000WO-EP07253.  
 XX 27-JUL-1999; 99DE-1035115.  
 PR 18-NOV-1999; 99DE-1055605.  
 PR 22-MAR-2000; 2000DE-1014085.  
 XX (BADI ) BASF AG.  
 PA Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R,  
 PI L1 Q;  
 DR WPI; 2001-182800/18.  
 PT Cytochrome P450 monooxygenase for oxidizing organic compounds, useful  
 especially for converting indole to indigo, has wide substrate range -  
 XX  
 PS Claim 5; Page -; 54pp; German.  
 XX The present sequence represents a modified cytochrome P450 monooxygenase.  
 CC The specification describes a modified cytochrome P450 monooxygenase  
 CC which can oxidize at least one of the following types of substrates:  
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics  
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or  
 CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or  
 CC optionally substituted cycloalkanes or cycloalkenes. The modified  
 CC cytochrome P450 monooxygenase are specifically used to oxidize indole  
 CC to indigo and indorubicin. However, they may be used to oxidise many  
 CC other substrates.  
 CC note: this sequence does not appear in the specification; it was created  
 CC using information provided.  
 XX  
 SQ Sequence 1048 AA;  
 Query Match 99.8%; Score 5444; DB 22; Length 1048;  
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TIKEMPOKTFEGELKPLPLNTDQKPVQALMKIADGEIPEKFAPRVTRYSORLIKE 60  
 DB 1 TIKEMPOKTFEGELKPLPLNTDQKPVQALMKIADGEIPEKFAPRVTRYSORLIKE 60  
 QY 61 ACDESFPDKLSQALKFVRDPAGDGLFTSWTEKMKKKAHNLPSFSQAMKGYHAMV 120  
 DB 61 ACDESFPDKLSQALKFVRDPAGDGLFTSWTEKMKKKAHNLPSFSQAMKGYHAMV 120  
 QY 121 DIAVOLVQKWERLNADDEHIEVPEDMTRLTDITGLCGFNRFNFSFRDQHPFTISWVRA 180  
 DB 121 DIAVOLVQKWERLNADDEHIEVPEDMTRLTDITGLCGFNRFNFSFRDQHPFTISWVRA 180  
 QY 181 LDEAMNKLOKRPANDDPPAYDENKROFOEDIKVMNDLVDKIIADKASGEGSDLLTHMLNG 240  
 DB 181 LDEAMNKLOKRPANDDPPAYDENKROFOEDIKVMNDLVDKIIADKASGEGSDLLTHMLNG 240  
 QY 241 KDPETGEPDLDENIRYQIITFLIAGHETTSGLLSFALYPLVKNPHYLQKAAEBAARVLVD 300  
 DB 241 KDPETGEPDLDENIRYQIITFLIAGHETTSGLLSFALYPLVKNPHYLQKAAEBAARVLVD 300  
 QY 301 PVSQYQVQKQKTYGVAVLNEALMLPTAPAFSLYAKEDTVLGSEYPLEKDELMVLIPOL 360  
 DB 301 PVSQYQVQKQKTYGVAVLNEALMLPTAPAFSLYAKEDTVLGSEYPLEKDELMVLIPOL 360  
 QY 361 HRDKTIWGDVVEEFPREFNPESAIPOHAFKPGNGORACIGQOFALHEATLVLMMLKH 420  
 DB 361 HRDKTIWGDVVEEFPREFNPESAIPOHAFKPGNGORACIGQOFALHEATLVLMMLKH 420  
 QY 421 FDFEDHTNYELDIKETLLKPEGFVYKAKSKKIPLGIPSPSTEQSAKKVKKAEANAHT 480  
 DB 421 FDFEDHTNYELDIKETLLKPEGFVYKAKSKKIPLGIPSPSTEQSAKKVKKAEANAHT 480  
 QY 481 PLVLVGSNMGTAEGRARLDADIAMSCKFAPQVATLDSHAGNIPRECAVLIIVASVNGHP 540  
 DB 481 PLVLVGSNMGTAEGRARLDADIAMSCKFAPQVATLDSHAGNIPRECAVLIIVASVNGHP 540  
 QY 541 PDNAKQFVMDLDOASADEVGVRSYFGCGDKMATTYQVPAFIDETLLAKKAENIADR 600  
 DB 541 PDNAKQFVMDLDOASADEVGVRSYFGCGDKMATTYQVPAFIDETLLAKKAENIADR 600  
 QY 601 GEADASDFEGTYEEMREHMSDVAAYFNLDIENSEDNKSTLSLOFVDSAADMLAMHG 660  
 DB 601 GEADASDFEGTYEEMREHMSDVAAYFNLDIENSEDNKSTLSLOFVDSAADMLAMHG 660  
 QY 661 AFSTNVVASKELDQPGSARSTRLEIELPREASVOEGDHLGVIPRNEGIVNVTARFGL 720  
 DB 661 AFSTNVVASKELDQPGSARSTRLEIELPREASVOEGDHLGVIPRNEGIVNVTARFGL 720  
 QY 721 DASQOIRLEAEEBEKLAHLPLAKTVSVLELQVYELQDPVTRTOLRAMAAKTVCPPHKEVL 780  
 DB 721 DASQOIRLEAEEBEKLAHLPLAKTVSVLELQVYELQDPVTRTOLRAMAAKTVCPPHKEVL 780  
 QY 781 EALLEKQAYKEQVLAKRLTMLLELEKYPACEMKFSERIALLPISRPYRYSISSPRVDEK 840  
 DB 781 EALLEKQAYKEQVLAKRLTMLLELEKYPACEMKFSERIALLPISRPYRYSISSPRVDEK 840  
 QY 841 QASITVSVSGEAMSGGEGEKGIAASNYLALQSGDITTCISTSPQSFITLPCXPBETPLIM 900  
 DB 841 QASITVSVSGEAMSGGEGEKGIAASNYLALQSGDITTCISTSPQSFITLPCXPBETPLIM 900  
 QY 901 VGPCTGVAPRFGVQARKOLKEGOSLGEAHLFGCRSPHEDLYOBELENAOSEGITTL 960  
 DB 901 VGPCTGVAPRFGVQARKOLKEGOSLGEAHLFGCRSPHEDLYOBELENAOSEGITTL 960  
 QY 961 HTAFSRMPNPKTYVQHVMEQDGKLLIELDQGAHFYICGDSQMAVAEATLMKSYADV 1020  
 DB 961 HTAFSRMPNPKTYVQHVMEQDGKLLIELDQGAHFYICGDSQMAVAEATLMKSYADV 1020  
 QY 1021 HOVSADARLMLQOLEEKGRAKDVWAG 1048  
 DB 1021 HOVSADARLMLQOLEEKGRAKDVWAG 1049

## RESULT 9

AAB31981

ID AAB31981 standard; Protein; 1048 AA.

AC AAB31981;

DT 15-MAY-2001 (first entry)

DE Amino acid sequence of a modified P450 monooxygenase protein.

KW Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubidin.

XX Bacillus megaterium.

FH Key Location/Qualifiers

FT Misc-difference 74 /note= "wild type Ala changed to Gly"

FT Misc-difference 87 /note= "wild type Phe changed to Val"

FT Misc-difference 188 /note= "wild type Leu changed to Gln"

PN WC00107630-A1.

PD 01-FEB-2001.

PF 27-JUL-2000; 2000MO-EP07253.

PR 27-JUL-1999; 99DE-1035115.

PR 18-NOV-1999; 99DE-1055605.

PR 22-MAR-2000; 2000DE-1014085.

PA (BADI ) BASF AG.

PI Hauser B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;

XX L1 Q;

XX WPI; 2001-162800/18.

XX Cytochrome P450 monooxygenase for oxidizing organic compounds, useful

XX especially for converting indole to indigo, has wide substrate range -

PS Claim 5; Page -; 54pp; German.

XX The present sequence represents a modified cytochrome P450 monooxygenase.

XX The specification describes a modified cytochrome P450 monooxygenase

XX which can oxidize at least one of the following types of substrates:

XX optionally substituted mono- or poly-cyclic aromatic heterocycles

XX containing nitrogen, sulphur or oxygen; optionally substituted mono- or

XX poly-cyclic aromatics; linear or branched alkanes or alkenes; or

XX optionally substituted cycloalkanes or cycloalkenes. The modified

XX cytochrome P450 monooxygenase are specifically used to oxidize indole

XX to indigo and indorubidin. However, they may be used to oxidise many

XX other substrates.

XX CC note: this sequence does not appear in the specification; it was created

XX using information provided.

XX Sequence 1048 AA;

XX Query Match 99.7%; Score 5440; DB 22; Length 1048;

XX Best Local Similarity 99.7%; Pred. No. 0;

XX Matches 1045; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 121 DIAVQVQKWERLNADENIEVPEDMTRLTLDITGLCGFNRYENSFYRDQPHPTSMVRA 180

DB 121 DIAVQVQKWERLNADENIEVPEDMTRLTLDITGLCGFNRYENSFYRDQPHPTSMVRA 180

QY 181 LDEANAKLQAPNDDPAYDENKQFQEDIRYNNNDVDKITADRKASGEQDDLLTHNLNG 240

DB 181 LDEANAKLQAPNDDPAYDENKQFQEDIRYNNNDVDKITADRKASGEQDDLLTHNLNG 240

QY 241 KDEPTEGPELDENIRYQIITFLIAGHETTSGLSFALYFLVKNPWHVQKAEEAARVLVD 300

DB 241 KDEPTEGPELDENIRYQIITFLIAGHETTSGLSFALYFLVKNPWHVQKAEEAARVLVD 300

QY 301 PVSYSQVQKQKTVGWNALNEALRLMPTAPAFSLYAKEDTVLGGSEYPLEKDELMVLLPOL 360

DB 301 PVSYSQVQKQKTVGWNALNEALRLMPTAPAFSLYAKEDTVLGGSEYPLEKDELMVLLPOL 360

QY 361 HRDKTIWGDVVEEFPFRFENPSAIPQAHAKPFGNGRACIGQOFALHEATLVLGWMLKH 420

DB 361 HRDKTIWGDVVEEFPFRFENPSAIPQAHAKPFGNGRACIGQOFALHEATLVLGWMLKH 420

QY 421 FDFEDHTNYELDIKETLTLLKPEGFVYKAKSKTILPGGIPSPSTEQSAKKYRKKAENAHNT 480

DB 421 FDFEDHTNYELDIKETLTLLKPEGFVYKAKSKTILPGGIPSPSTEQSAKKYRKKAENAHNT 480

QY 481 PLLVLGSSNMGTAEATADLADLAMSKGAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540

DB 481 PLLVLGSSNMGTAEATADLADLAMSKGAPQVATLDSHAGNLPREGAVLIVTASYNGHP 540

QY 541 PDNAKQFVMDLQASADEVKGVRYSVFGCGDKWATTYQGVPAFIDETTLAKAGENIADR 600

DB 541 PDNAKQFVMDLQASADEVKGVRYSVFGCGDKWATTYQGVPAFIDETTLAKAGENIADR 600

QY 601 GEADASDPFEGTYBEKREHMSDVAAYFNLDIENSEDNKSTLSLOFVDSAADPLAMHMG 660

DB 601 GEADASDPFEGTYBEKREHMSDVAAYFNLDIENSEDNKSTLSLOFVDSAADPLAMHMG 660

QY 661 AFSITNVASKELQOPGASRSTRHLEIELPREASVOEGDHLGVIPRNYEGIVNRVTARFGL 720

DB 661 AFSITNVASKELQOPGASRSTRHLEIELPREASVOEGDHLGVIPRNYEGIVNRVTARFGL 720

QY 721 DASQOIRLEABEERKLHLPLAKTVSVBELLYVELDQPVTRTQIRAMAATVCPPHVEEL 780

DB 721 DASQOIRLEABEERKLHLPLAKTVSVBELLYVELDQPVTRTQIRAMAATVCPPHVEEL 780

QY 781 EALLEKQAYKEOVLAKRLTMLLELEKYPACEMKPSERIALPSPRPYSSISSPRYDEK 840

DB 781 EALLEKQAYKEOVLAKRLTMLLELEKYPACEMKPSERIALPSPRPYSSISSPRYDEK 840

QY 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPOSEFTLPKDPETPLIM 900

DB 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPOSEFTLPKDPETPLIM 900

QY 901 VGGTGVAPPRGFGVQARKOLKEQOQSIGEAHLVFGCRSPHEDYLYOBELNAGSEGIITL 960

DB 901 VGGTGVAPPRGFGVQARKOLKEQOQSIGEAHLVFGCRSPHEDYLYOBELNAGSEGIITL 960

QY 961 HTFSPRMPNPKTYVQVHVMQDCKLIELDQAHFVTCGDSGOMARAVATLTKMSYADV 1020

DB 961 HTFSPRMPNPKTYVQVHVMQDCKLIELDQAHFVTCGDSGOMARAVATLTKMSYADV 1020

QY 1021 HOVSEADARLMLQOLEKGRYAKDVWAG 1048

DB 1021 HOVSEADARLMLQOLEKGRYAKDVWAG 1048

## RESULT 10

AAR11604

ID AAR11604 standard; Protein; 1085 AA.

XX AAR11604;

XX 20-JUN-1991 (first entry)

DE P450 17-alpha/P450 BM-3 fusion protein.  
 XX bovine adrenal; cytochrome P450; oxidase; reductase; steroid;  
 KW plasmid p(alphabM1).  
 XX JF03061490-A.  
 XX PD 18-MAR-1991.  
 XX PF 28-JUL-1989; 89JP-0197296.  
 XX PR 28-JUL-1989; 89JP-0197296.  
 XX PA (SUMO) SUMITOMO CHEM IND KK.  
 XX DR WPI; 1991-121848/17.  
 XX DR N-PSDB; AA011474.  
 XX PT P450 reductase fused oxidase coding gene - has both mono-atomic  
 PT oxygenation activity of bovine adrenal cytochrome p450 17-alpha  
 PT and reductivity supplying activity  
 XX  
 PS Claim 1; Fig 2; 8pp; Japanese.  
 CC The protein is a fusion of bovine adrenal cytochrome P450 17-alpha  
 CC and Bacillus megaterium-derived cytochrome P450 BM-3. The fusion  
 CC protein has the monatomic oxygenation activity of the former and  
 CC the reductivity supplying activity of the latter. Plasmid p(alphabM1),  
 CC containing the recombinant sequence encoding the fusion protein, is  
 CC used to transform *Saccharomyces cerevisiae*. The transformant is  
 CC designated AH22(p(alphabM-1)) and can be used for the synthesis of  
 CC steroids.  
 XX  
 SQ Sequence 1085 AA;  
 Query Match 57.8%; Score 3154.5; DB 12; Length 1085;  
 Best Local Similarity 60.9%; Pred. No. 1.2e-211;  
 Matches 672; Conservative 105; Mismatches 222; Indels 105; Gaps 21;

DB 470 DGKLPSELEHSHASVLQKPKFKVKEVRQ-----AKKEQAQAGSIFPGTAENAHNTPLV 522  
 QY 485 LYGSNMGTAGTARLADIAMSKGAPQVATLDSHAGNLPRREGAVLITVASNGHPDNA 544  
 DB 523 LYGSNMGTAGTARLADIAMSKGAPQVATLDSHAGNLPRREGAVLITVASNGHPDNA 582  
 QY 545 KQFVMDLOASADEVKGVRSVFCGDKMATTYQKVPAPIDETLAKGAENIADRGAD 604  
 DB 583 KQFVMDLOASADEVKGVRSVFCGDKMATTYQKVPAPIDETLAKGAENIADRGAD 642  
 QY 605 ASDDFEGTYEEMKEMHMSDVAATFNLDIENSEDKSTLSQFVDSADMDLAKHGAFT 664  
 DB 643 ASDDFEGTYEEMKEMHMSDVAATFNLDIENSEDKSTLSQFVDSADMDLAKHGAFT 702  
 QY 665 NVVASKELOQGSARSTRHLEIELEPKASVQEGDHLGVIPRNEGYVNRVTARFGDASQ 724  
 DB 703 NVVASKELOQGSARSTRHLEIELEPKASVQEGDHLGVIPRNEGYVNRVTARFGDASQ 762  
 QY 725 QIRLEAEKEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAARTVCPKHVELEALL 784  
 DB 763 QIRLEAEKEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAMAARTVCPKHVELEALL 822  
 QY 785 EKQAYKQVUAKRLTMLELEKYPACEMKSEFTALLPSTRPRYSSISSPRVDEKQAS 844  
 DB 823 EKQAYKQVUAKRLTMLELEKYPACEMKSEFTALLPSTRPRYSSISSPRVDEKQAS 882  
 QY 845 TVSVSGEAMSGYGEYKGIASNYLAELQEGDTITCFSTPQSEFTLPKQDEFTLIMWPG 904  
 DB 883 TVSVSGEAMSGYGEYKGIASNYLAELQEGDTITCFSTPQSEFTLPKQDEFTLIMWPG 942  
 QY 905 TGVAFFRGVQARKOLKEQGSQSGEALHYFGCSPHEDVLYQSELENAQSEGIITHTAF 964  
 DB 943 TGVAFFRGVQARKOLKEQGSQSGEALHYFGCSPHEDVLYQSELENAQSEGIITHTAF 1002  
 QY 965 SRMPOKTYVQVQVMEQDKLIELDQGNHFTICGSGQMAPAVENTLTKSYADVQVS 1024  
 DB 1003 SRMPOKTYVQVQVMEQDKLIELDQGNHFTICGSGQMAPAVENTLTKSYADVQVS 1062  
 QY 1025 EADARLWLOOLEEKRYAKDVWAG 1048  
 DB 1063 EADARLWLOOLEEKRYAKDVWAG 1085

RESULT 11  
 AAP81334  
 ID AAP81334 standard; protein; 1144 AA.  
 AC AAP81334;  
 DT 19-OCT-1990 (first entry)  
 XX  
 DE Expression prod. of plasmid pAMP19.  
 XX  
 KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;  
 KW industrial waste.  
 XX  
 PN JF63044888-A.  
 XX  
 PD 25-FEB-1988.  
 XX  
 PF 12-AUG-1986; 86JP-0187713.  
 XX  
 PR 12-AUG-1986; 86JP-0187713.  
 XX  
 PA (AGEN) AGENCY OF IND SCI TECH.  
 XX  
 DR WPI; 1988-094816/14.  
 DR N-PSDB; AAN81743.  
 XX  
 PT Chimeric fusion enzyme gene - coding oxidation enzyme of cytochrome p-450  
 PT and NADPH-cytochrome p-450 reduction enzyme  
 XX  
 PS Disclosure; ; P; Japanese.



XX See also AAN81744-48.  
 CC  
 XX  
 SQ Sequence 1144 AA;  
 Query Match 17.8%; Score 971.5; DB 9; Length 1144;  
 Best Local Similarity 28.3%; Pred. No. 7,4e-59;  
 Matches 320; Conservative 186; Mismatches 468; Indels 157; Gaps 43;  
 25 PVQALMKIADLGEIIFKFEAPGRTVRLSSQRLIKACDSRDKLSQALKFVRDPAGD 84  
 DB PHLSLTKLSQOYGDVLIQIRIGSTPVVLSGLMTIKQA-----LVKGGDPFKGR 110  
 63 GLFTSWTHEKN-----WKKAHNILLPSFSQAMKGY-----HA 117  
 85 GLFTSWTHEKN-----WKKAHNILLPSFSQAMKGY-----HA 117  
 DB PDLYSFTLLANGSGMTFNPDSGFLMAARRL-----AQNMLKSFASIASDPTLASCYLEE 165  
 111 PDLYSFTLLANGSGMTFNPDSGFLMAARRL-----AQNMLKSFASIASDPTLASCYLEE 165  
 QY 118 MMYDIAVOLVOKERLNAD-EHIEVEDMTRLTLDITGLCGFNYRNSFYRDPHPFITS 176  
 DB HVSKEAEYLLSKFKQKMAEYGHDPFKYLVSVAANYICAICFGRYD--HDDQELSLIVN 223  
 166 HVSKEAEYLLSKFKQKMAEYGHDPFKYLVSVAANYICAICFGRYD--HDDQELSLIVN 223  
 QY 177 MYVALDEAMNK-----LQRPND--DPAVDENKROFQEDIKVNDLVDKTIADRKA 225  
 DB 224 LSNFEGSVTSGYPADFIPLIRYLPNSSLDAPKDLNKKFY-----SEMKKLIIKENHYR 275  
 224 LSNFEGSVTSGYPADFIPLIRYLPNSSLDAPKDLNKKFY-----SEMKKLIIKENHYR 275  
 QY 226 SGEQ-----SDLLTHMLNGK--DPEETGEPLDENIRYQIITFLIAGHETTSGLSPALY 278  
 DB 276 TFEKGHIRDTTDLIEHCQDRDENANNVQLSDKVTITVFGLGAFDITTAISWSLM 335  
 276 TFEKGHIRDTTDLIEHCQDRDENANNVQLSDKVTITVFGLGAFDITTAISWSLM 335  
 QY 279 FLVKNPHVLQKAEEAARVL--VDPVPSYKQVKQIKYGVNLNEALRLMPTAPAFSL--YA 335  
 DB 336 YLVTNPIRIQKIOBELDTVIGRDRQPLSDRQPLYLEAFILETFRHSFVP--FTIPHSY 394  
 336 YLVTNPIRIQKIOBELDTVIGRDRQPLSDRQPLYLEAFILETFRHSFVP--FTIPHSY 394  
 QY 336 KEDTVLGEYELPKGBELMLLIPQHRDKITMGDVEEPREPPENS-AIPQHAEP-- 392  
 DB 395 IRDTSLNGFY-IRKGHCVFNQOVNHDQELMGP-NEFRPERLTSGLTDKHLSEKVI 452  
 395 IRDTSLNGFY-IRKGHCVFNQOVNHDQELMGP-NEFRPERLTSGLTDKHLSEKVI 452  
 QY 393 -FGNGORACIGOOFALEATLVLMMLKHPDFEDHTYEALDIKET--LTLPK--EGFVV 446  
 DB 453 LFLGLGRKCIIGETIGRELVFLAILIQMEFNVSPBEKXDMTPAYGLTIKARCHEFQV 512  
 453 LFLGLGRKCIIGETIGRELVFLAILIQMEFNVSPBEKXDMTPAYGLTIKARCHEFQV 512  
 QY 447 KAKSK--KIPLGGIPEPSTEQS-AKKYRKAEANMNTPLVLYGSNGTAEGTARDIADI 503  
 DB 513 QMRSSGPRAMIQTAPPEKSSFEKMKKTGRN-----IIVFGSSQGTAEFEFANRLSKD 567  
 513 QMRSSGPRAMIQTAPPEKSSFEKMKKTGRN-----IIVFGSSQGTAEFEFANRLSKD 567  
 QY 504 AMSKGAPOVATIDSH---AGNLPR--EGAVLITVASY-NGHPNDNAKPFVMDLQASA 556  
 DB 568 AHRYGMRKMSADPEEYDLADLSLPEIDKSLVVFQMTYEGEGDPTDAODFYWMLQETDV 627  
 568 AHRYGMRKMSADPEEYDLADLSLPEIDKSLVVFQMTYEGEGDPTDAODFYWMLQETDV 627  
 QY 557 DEYKGVRSYVFGCGDKMMATTYQKVP--FIDETLLAKGAENIADGADADDFEGTY 613  
 DB 628 D-LTGKVFAGFGLGNK---TYEHFNAMGKYVDORLEQLQGRIFELGLDDGDNLEEDF 682  
 628 D-LTGKVFAGFGLGNK---TYEHFNAMGKYVDORLEQLQGRIFELGLDDGDNLEEDF 682  
 QY 614 EEWREHMSDVAAYFNLDIENSDNKSTLSLQFVDSADMPAKM----- 659  
 DB 683 ITRREQFWPAPVCEFFGVEATGEESIRQYELVYHE--DMDVAKVYVYGMGRILKSYENOK 739  
 683 ITRREQFWPAPVCEFFGVEATGEESIRQYELVYHE--DMDVAKVYVYGMGRILKSYENOK 739  
 QY 660 -----GAFSTNVASGELOQPGASARSTRLEIEL-PKEASVQEGHLYGIPRYBSIVN 712  
 DB 740 PEPDANKPFLAAVYANKLNQ--GTERHLMLELDIISDKIRYBSGDAVVAAYPANDSALVN 798  
 740 PEPDANKPFLAAVYANKLNQ--GTERHLMLELDIISDKIRYBSGDAVVAAYPANDSALVN 798  
 QY 713 RVTARFG--LDASQOIRLEAEKEKLAHLPLAKTVSEBELQYVLODPVTRTOLRAAAK 770  
 DB 799 QIIEILGADLDVMSLNNDDEESNKGIPFCPTTYRALTYYLDTINP-PRTNVLYLAQ 857  
 799 QIIEILGADLDVMSLNNDDEESNKGIPFCPTTYRALTYYLDTINP-PRTNVLYLAQ 857  
 QY 771 TVCP-----HKVEELALLEKQAYKQVLAKRLTMLLEKYPACEMKSEFIALPST 824  
 DB 858 YASEPSEOEHLKMASSSGGKELYLSMVVEARHILAILODYPSLRPPIDLCELLPRL 917  
 858 YASEPSEOEHLKMASSSGGKELYLSMVVEARHILAILODYPSLRPPIDLCELLPRL 917  
 QY 825 RPYYSSTSSPRVDEKASITVSVSGEAMSGYGEYGIASNYL--ALQGGDT-----IT 878  
 DB 918 QARYSTASSKVPNSVHI CAVAVEYEAQSGRVN-KGVATSWLRAPKAPENGGRALVP 976  
 918 QARYSTASSKVPNSVHI CAVAVEYEAQSGRVN-KGVATSWLRAPKAPENGGRALVP 976

QY 879 CFISTPQSEFTLEKDEDEPLINVGPGTGVAPFEGFVQARKOLKEQSGSLGEAHLFYGCRS 938  
 DB 977 MFVR--KSQERLPFKSTTPVIMVPGTGIAPFWMGFIQERAMLEBQGEVGETLLYYGCRR 1034  
 977 MFVR--KSQERLPFKSTTPVIMVPGTGIAPFWMGFIQERAMLEBQGEVGETLLYYGCRR 1034  
 QY 939 PHEDIYQSELENAQSEGIIT-LHTAFSRMPNPKTYVQHWQDQKLLIELDQ-GAHF 996  
 DB 1035 SDDYLYREELARFHHQDGLTQLVNAFSR-EQAHKYVQHLRLRDREHMLKLIHEGGAHI 1093  
 1035 SDDYLYREELARFHHQDGLTQLVNAFSR-EQAHKYVQHLRLRDREHMLKLIHEGGAHI 1093  
 QY 997 YICGDSQMAPVATEATLMKSYADVQVSEADARLMTQOLEEKGRYAKDWVA 1047  
 DB 1094 YVCGDARNNAKDVQNTFYDIVAEFGPEMHTQADVYKKLMTKGRISLDVMS 1144  
 1094 YVCGDARNNAKDVQNTFYDIVAEFGPEMHTQADVYKKLMTKGRISLDVMS 1144  
 RESULT 12  
 AAP81337  
 ID AAP81337 standard; protein; 1150 AA.  
 XX  
 AC AAP81337;  
 XX  
 DT 19-OCT-1990 (first entry)  
 XX  
 DE Expression prod. of plasmid pALP25.  
 XX  
 KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;  
 KW industrial waste.  
 XX  
 PN JP63044888-A.  
 XX  
 PD 25-FEB-1988.  
 XX  
 PF 12-AUG-1986; 86GP-0187713.  
 XX  
 PR 12-AUG-1986; 86GP-0187713.  
 XX  
 PA (AGEN ) AGENCY OF IND SCI TECH.  
 XX  
 DR WPI; 1988-094816/14.  
 XX  
 DR N-PSDB; AAN81746.  
 XX  
 PT Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450  
 PT and NADPH-cytochrome p-450 reduction enzyme  
 XX  
 PS Disclosure; ; p; Japanese.  
 XX  
 CC See also AAN81743-85 and AAN81747-48.  
 CC  
 XX  
 SQ Sequence 1150 AA;  
 Query Match 17.7%; Score 968.5; DB 9; Length 1150;  
 Best Local Similarity 28.1%; Pred. No. 1.2e-58;  
 Matches 320; Conservative 166; Mismatches 468; Indels 163; Gaps 43;  
 25 PVQALMKIADLGEIIFKFEAPGRTVRLSSQRLIKACDSRDKLSQALKFVRDPAGD 84  
 DB 63 PHLSLTKLSQOYGDVLIQIRIGSTPVVLSGLMTIKQA-----LVKGGDPFKGR 110  
 63 PHLSLTKLSQOYGDVLIQIRIGSTPVVLSGLMTIKQA-----LVKGGDPFKGR 110  
 QY 85 GLFTSWTHEKN-----WKKAHNILLPSFSQAMKGY-----HA 117  
 DB 111 PDLYSFTLLANGSGMTFNPDSGFLMAARRL-----AQNMLKSFASIASDPTLASCYLEE 165  
 111 PDLYSFTLLANGSGMTFNPDSGFLMAARRL-----AQNMLKSFASIASDPTLASCYLEE 165  
 QY 118 MMYDIAVOLVOKERLNAD-EHIEVEDMTRLTLDITGLCGFNYRNSFYRDPHPFITS 176  
 DB 166 HVSKEAEYLLSKFKQKMAEYGHDPFKYLVSVAANYICAICFGRYD--HDDQELSLIVN 223  
 166 HVSKEAEYLLSKFKQKMAEYGHDPFKYLVSVAANYICAICFGRYD--HDDQELSLIVN 223  
 QY 177 MYVALDEAMNK-----LQRPND--DPAVDENKROFQEDIKVNDLVDKTIADRKA 225  
 DB 224 LSNFEGSVTSGYPADFIPLIRYLPNSSLDAPKDLNKKFY-----SEMKKLIIKENHYR 275  
 224 LSNFEGSVTSGYPADFIPLIRYLPNSSLDAPKDLNKKFY-----SEMKKLIIKENHYR 275  
 QY 226 SGEQ-----SDLLTHMLNGK--DPEETGEPLDENIRYQIITFLIAGHETTSGLSPALY 278  
 DB 276 TFEKGHIRDTTDLIEHCQDRDENANNVQLSDKVTITVFGLGAFDITTAISWSLM 335  
 276 TFEKGHIRDTTDLIEHCQDRDENANNVQLSDKVTITVFGLGAFDITTAISWSLM 335  
 QY 279 FLVKNPHVLQKAEEAARVL--VDPVPSYKQVKQIKYGVNLNEALRLMPTAPAFSL--YA 335  
 279 FLVKNPHVLQKAEEAARVL--VDPVPSYKQVKQIKYGVNLNEALRLMPTAPAFSL--YA 335



QY 707 YEGIVNVTARFG--LDASQOIRLEAESEKLAHLPLAKTVSVEELLQYVELODPVETQOL 764  
 DB 799 DSALVNOIGELGADLDVIMSLNLDSESNKGFPPCPTTYRTALTYLDTINP--PRTNV 857  
 QY 765 RAMAAKTVCP-----HKVELEALLKQAYKEOVLAKRLTMELEKEYPACEMKFEFTI 818  
 DB 858 LYELAQVASEBSEOEHLHKAASSSGEKELEYLSWVVEARRHIILALDDYSLRPPIDHLC 917  
 QY 819 ALPSIRPYRYSISSSPRVDEKQASITVSVSGEAMSGYGEYKGIASNVY--AEIQEGDT- 876  
 DB 918 ELPLRLARYSIASSSSKVHPNSVHICAVAVEYAKSGRVN--KGVATSWLPAKPAENG 976  
 QY 877 -----ITCFISTPOSEFTLPKDPETPLIMVGPSTGVAFPGFVQARKOLKEQOSLGEAHL 932  
 DB 977 GRALVMEFVR--KSQFRLPFKSTTPVIMVGPSTGVAFPGFVQARKOLKEQOSLGEAHL 1034  
 QY 933 YFGCRSHEDYLYOELEENAOSEGIT--LHTAFSRMNPQKTYQVHMEODGKKLIELLD 991  
 DB 1035 YGGRSRDEBYLYREELARPHKDGALTQLVNAFPR--EQAHKVVYQHLKEDREHLMKLIH 1093  
 QY 992 Q-GAHFYICGDSQMAPAVEATLMKSYADYHQSADARLMLQOLEKGRYAKDYMA 1047  
 DB 1094 EGGHIIYVCGDARMNAKOVNTFYDVAEFGPMETHQAVDYVKLMTKGRISLDVWS 1150

## RESULT 14

ID AAP81336 standard; protein; 1162 AA.  
 AAP81336

XX AC AAP81336;  
 XX DT 19-OCT-1990 (first entry)  
 DE Expression prod. of plasmid pALP17.  
 KW Cytochrome P450; NADPH cytochrome P-450; reduction; oxidation;  
 KW Industrial waste.  
 XX PN JP63044888-A.  
 XX PD 25-FEB-1988.  
 XX PF 12-AUG-1986; 86JP-0187713.  
 XX PR 12-AUG-1986; 86JP-0187713.  
 XX PA (AGEN ) AGENCY OF IND SCI TECH.  
 XX DR WPI; 1988-094816/14.  
 XX DR N-PDB; AAN81745.  
 PT Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome P-450  
 XX and NADPH-cytochrome P-450 reduction enzyme  
 XX Disclosure; ; P; Japanese.  
 XX See also AAN81743-84 and AAN81746-48.  
 SQ Sequence 1162 AA;

Query Match 16.8%; Score 916.5; DB 9; Length 1162;  
 Best Local Similarity 27.2%; Pred. No. 5.3e-55;  
 Matches 314; Conservative 185; Mismatches 469; Indels 187; Gaps 43;  
 QY 25 PVQAMKIALDELGEIFEFAPKRVTRKLSORLIKEACDSRPDKNISQALKFYRPAQD 84  
 DB 63 PHLSTLTLSQOYGVDLQIRIGSTPVVVLSGINTIKQA-----LVKQGDFFKGR 110  
 QY 85 GLFTSWTHEKN-----WKAHNIILPSFGQAMKGY-----HA 117  
 DB 111 PDLYSTFLINAGSMTNPDSPGLMAARRL-----AQNALKSFSTIASDPTLASSCYLEE 165

QY 118 MVDIAVOLVQKMERLNAD-EHIEVEDMTRLTLDTGLCGFNVRNFSFYRQDPHPETIS 176  
 DB 166 HVSKEAEYLSKQGLMAEVGHDFPKYLVSVANVICAICFGRRD--HDDQELLSTVN 223  
 QY 177 MPALDEANMK-----LQANPD--DPAYENKQFOEDIKVNNDLVDKILADRA 225  
 DB 224 LSNFEFGVSSGYPADFIPLIRYLPNSSLDAFDLKNKFY-----SFMKTLIKHYR 275  
 QY 226 SGEQ-----SDLLTLMNGK--DPETGEPLDDENIROYQITFLIGHETTSGLSALY 278  
 DB 276 TFEKGHTRDITDLIEHCQDRIDENANVOLSDCKYITTFDLPGAQEDTITTAISWSLM 335  
 QY 279 FLVKNPHVLQKAEEARVYL--VDPVSYKQVKOLKTYGWLNALRLMPAPAFSL--YA 335  
 DB 336 YLVTRNRIOKQIEBLDTVIGRDRPRLSDRPLPIEAFLITFRHSSVP--FTIPHST 394  
 QY 336 KEDTVYGGEPLEKGBELMYLIPQLHRDKTIWGDVVEEFPERPENPS-AIPQHAEPK- 392  
 DB 395 IRDTSLNGFY-IRKGHCVFNQWQVNHDDQELMGDP--NEFPERFLLTSSGTLDKHLSKVI 452  
 QY 393 -FNGSORACTIGQOFALHEATLVLMMLKHPDEFDHNNYELDIKET--LTLKP--EGFVY 446  
 DB 453 LPELGRKRCIGETIGLEVFLLFLLIQMEFNVSPEEKVMTPAYGLTLKHARCEHFQV 512  
 QY 447 KAKSKKIPLGGLPSPESTQSA-----KVKRKAENAHNT 480  
 DB 513 QKRS-----SGRPSAAARSAARSAARSAARSAARSAARSAARSAARSAARSAARSAAR 563  
 QY 481 PLIVLYGSMNGIAEGTARDLADIAMSKGPAQVATLDSH--AGNLPR--EBAVLIVTA 534  
 DB 564 -IIVFYGSQGTAEERFANRLSKDHRVYGMKMGADDEEYDLADLSLPEIDKLVFVCM 622  
 QY 535 SY-NGHPNDNAKQVFMLODASADEYKVRYSVFGGDKNMATYQKVP--FIETTLA 590  
 DB 623 TYEGEDPTDVAQFYMLQETDVT--LTVGFAVFGJANK--TYEFNMGMKTYVQORLE 677  
 QY 591 AKGAENIADRGEDASDDEGTYEWRERHMSDVAAVFNLDIENSDNKSTLSLOEFD 650  
 DB 678 QLGAGRIIFELGLDDDGNEEDFTITWBOFWPAVCFEGVEATGESSIRQYLVVHE-- 735  
 QY 651 ADMPLAKM-----GASTNVASKELOQPGSARSTRHLEL-P 689  
 DB 736 -DMDVAKVYTGEMGRKLSYENQKRPDPANPFLLAATYANKLNQ--GTERHMLHELIDIS 793  
 QY 690 KEASYOEGHLYGTPENYEGIVNVTARFG--LDASQOIRLEAESEKLAHLPLAKTVSVE 747  
 DB 794 SKTRYESGDHVAAYPANDSALVNOIGELGADLDVIMSLNLDSESNKGFPPCPTTYRT 853  
 QY 748 ELQYVELDPVYRTOLRAMAAKTVCP-----HKVELEALLKQAYKEOVLAKRLTML 801  
 DB 854 ALTYVYLDITNP--PRTNVLYELAEYASEBSEOEHLHKAASSSGEKELEYLSWVVEARRHL 912  
 QY 802 ELIEKYPACEMKFEFTIALPSIRPYRYSISSSPRVDEKQASITVSVSGEAMSGYGEYK 861  
 DB 913 AIIQDYPSPRLPIDHLCBLPRLQARYSIIASSSKVHPNSVHICAVAVEYAKSGRVN--K 971  
 QY 862 GIASNYL--AEIQEGDT-----ITCFISTPOSEFTLPKDPETPLIMVGPSTGVAFPGFVQ 915  
 DB 972 GVATSWLRAKEPAGENGRLVPMFVR--KSQFRLPFKSTTPVIMVGPSTGVAFPGFVQ 1029  
 QY 916 ARKOLKEQOSLGEAHLFYGCRSHEDYLYOELEENAOSEGIT--LHTAFSRMNPQKTY 974  
 DB 1030 ERMVMEQKQEVETILLYGCRSDSDYLYREELARPHKDGALTQLVNAFSSRSDSDYLY 1089  
 QY 975 VQHV--MEODGKKLIELDOGAHFYICGDSQMAPAVEATLMKSYADYHQSADARLML 1032  
 DB 1090 REELARFHKDG--ALTOLVNVAFSIYVCGDARMNAKOVNTFYDVAEFGPMETHQAVDY 1147  
 QY 1033 OOLEEKGRYAKDYMA 1047  
 DB 1148 KKLMTKGRISLDVWS 1162

```

RESULT 15.
AAP81338
ID AAP81338 standard; protein, 1132 AA.
XX
AC AAP81338;
XX
DT 19-OCT-1990 (first entry)
DE Expression prod. of plasmid pALP4.
XX
KM Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;
XX industrial waste.
XX
FN JPe3044888-A.
XX
PD 25-FEB-1988.
XX
PF 12-AUG-1986; 86JP-0187713.
XX
PR 12-AUG-1986; 86JP-0187713.
XX
PA (AGEN ) AGENCY OF IND SCI TECH.
XX
DR WPI; 1988-094816/14.
XX
DR N-PSDB; AAN81747.
XX
PT Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450
PT and NADPH-cytochrome p-450 reduction enzyme
XX
PS Disclosure; ; Japanese.
XX
CC See also AAN81743-86and AAN81748.
XX
SQ Sequence 1132 AA;

Query Match 16.6%; Score 906.5; DB 9; Length 1132;
Beet Local Similarity 27.2%; Pred. No. 2.6e-54;
Matches 308; Conservative 187; Mismatches 464; Indels 175; Gaps 44;

25 PVQALMKIADLGEIFKEAPGRVTRVYSQRLTKKACDESRFDKNSQALKFVDFPGD 84
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
63 PHLSTKLSQOYGDVLQIRIGSTPVVLSGLNTIKQA-----LVKQGDDEKGR 110
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
85 GLFTSWTHEKN-----WKAHNLILSFSSQAMKGY-----HA 117
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
111 PDLSFTLIANGQSGTWPNDSGPLMAARRL-----AGNALKSPISADPTLASSCYLE 165
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
118 MMVDIAVOLVOKMERLND-EHIEVEDMTRLTDTGLCGNFRNSFYRDQPHPTTS 176
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
166 HVSKEAEYLISKFOKLMAEVGHFDPFKYLVSVANVICAICFGRYD--HDDQELSLVN 223
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
177 MVRALDEAMNK-----LORAND---DPAVDENKQFOEDIKVMNDLVDKIADKA 225
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
224 LSNREGVETSGGYPADFPILIRKYLPNSSLDAPKDLNKKFY-----SEFKLKEHYR 275
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
226 SGEQ-----SDDLITMLNGK-DPETGEPLDENIRYQITFLIAGHETTSGLISFALY 278
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
276 TFEKGHTRIDTSLIEHQDRDENANVQLSDDKVITIVFDLPGAGFDITTTAISWLM 335
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
279 FLVKNPHVLQRAAEAAVYL-VDPVSYKQVKQLKYGMVINEALRLMPTAPASL--YA 335
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
336 YLVNPRIRQIKIOELDTVIGDRPRLSDRPQLYLEAFILFETFRHSSFVP-FTIPHS 394
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
336 KEDTVLGEVYLEKDELMVLIPQLHRDKTIWGDVEEFRRPERFNP--AIPQAFKP-- 392
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
395 IRDTSLNNGFY-IPKGHCVFNQWQVNDHDELWGP-NFRRERFLTSSGTLDKHSEKQM 452
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
393 ---FGNGORACIGQFALHEATLVLGMMLKHFDEFEDHTNYELDIKETTILKPEGFV-- 446
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
453 EFNNSPGEK-----DWTIRAGLTLKARCB--HFQVQMRSS---GPRAAAAARA 497
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
447 -----KAKSKKIPLGGIIPSPSTEOS-AKVRKKAENAHNTPLVLVYGSNMGTAEGTADL 500
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Db 498 AADRAAADAARAMIQTAPPVKSSFEVKKKKTGRN-----IIVFGSQGTAEFANRL 552
Oy 501 ADIAMSKEFAPQVATLDSH-----AGNLPR--EGAVLIVTASY-NGHPDNAKQFVDLQ 553
Db 553 SKDHRGIRGMSADPREYDLADLSLPEIDKSLVFCMTYGEGBPTDAQDFYDLQ 612
Oy 554 ASADENVKRVYSVFGCGDKXWATTYQKVA--FIDETLAKEAENIADRGEDASDFE 610
Db 613 TDVD-LTGKFAVFGJGNK-----TYEHFNAMGKYVDQRLQAGQRIFFELGLDDDDGNLE 667
Oy 611 GTYEEMREHMSVDAAFENLDIENSEDNKSTLSLQFVDSAADPPLAMH----- 659
Db 668 EDFITWREQFWPAVCEFFGEATGEBSINQYELVHE--DMDVAKVYTGEMRLKSYE 724
Oy 660 -----GAFSTNVVASKELOPGSARSTRHLEIL-PKASVYOCGDHAGVPRNYEG 709
Db 725 NQKPPDAPKPPFLAAVYANKLNQ-GTERILMHELDISDKIRYESGDHVAAYPANDSA 783
Oy 710 IYNRVTAFIG--LDAQOIRLEAEKEKLAHLPLAKTVSVEELLQYVELQDPVTRTQLRAM 767
Db 784 LVNQIGETLADLDVIMSLNNLDESNKKHPCPCTYRTALTYLDTNP-PRTNVLYE 842
Oy 768 AKTVCP-----HKVELALBEKQAYKEQVLAKLTMLELEKYPACEMKSEFIALL 821
Db 843 LAQYASEPSEOEHLKXVASSGEGKELYLSWVVEARRHILAILQDPSLRPPIDHLCCELL 902
Oy 822 PSIRPRYYSISSPRVDEKQASITVSVSGEAMSGYGEYGIASNYL-AELOEGDT----- 876
Db 903 PRLOARYTSLASSKHPNSVHICAVAVEYEAASGRN-KGVATSWLRAEPAGENGRA 961
Oy 877 -ITCFISTPOSEFTLPKDPETPLIMVPGTGVAAPFRGFVQARKOLKEQOGLBAHLFYG 935
Db 962 LVPMFVR--KSQFRLPFKSTTPVIMVGPGTGIAIPFMGFIQERAMLRQGEVETLLYYG 1019
Oy 936 CRSPHEHYLYOEHELENAQSGIIT-LHTASRPNOKPTVQVQHMEDDGKLLIELDQ-G 993
Db 1020 CRSDDEDYLYREBELARPHKQDGLTLQNVAFSR-EQAKVYVQHLKKDRHELMKLIHEGG 1078
Oy 994 AHFYICGDSQMAPAVEATLMKSYADVHVQSEADARLMLQOLEBKGRYADVNA 1047
Db 1079 AHIVCGDARMAKDVONTFYDVAERGPMEHQAVDYVKKLMTKGRISLDVNS 1132

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Search completed: May 29, 2003, 10:04:08  
Job time : 82 secs



Db 300 LALAAHSDATEADRLQFLASREKDEYAEWIVANORSILLEWEAFPSAKEPLGVFPAI 359  
 QY 821 LPSIRPYVSISSSPVDEKQASTIVSVSGEAMSGVEYKIASNY-----LAEIOEG 874  
 Db 360 APRLOPRTYSSSSPKVNPRIHVTCALVY-EKTPGGRIRHKGICSTWKAVALPLENDQC 418  
 QY 875 DTTCFISTPOSEFTLPKDPETPLIMVPGTVA-PFRGFVQARKOLKEOGSLGEAHLVF 934  
 Db 419 SSAPIFVRT--SNRRLPADPKVPIVMIGPTGLAPFGGFLQERLALKESTGELQSTLFF 476  
 QY 935 GCRPHEDYLYQELLENANOSGITT-LHTASRNPNOPTKYVQVYMEDQKLIJELDDG 993  
 Db 477 GCRNRKVDIFIEYNELNFEVNGALSELDMAFSR-EGASKEYVQHKMSQKSDINMMLSEG 535  
 QY 994 AHFICGSGQMAVAEATLMKSYADVHVQSEADARLMLQOLEKGRYAKDVW 1046  
 Db 536 AYLVCGDAKAMADVHTLHTIVQEGNLDSKALYVKVLQMSGRILRDVW 588

## RESULT 2

US-07-642-002-2  
 ; Sequence 2, Application US/07642002  
 ; Patent No. 5268465  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bredt, David S.  
 ; APPLICANT: Hwang, Paul M.  
 ; APPLICANT: Reed, Randall  
 ; APPLICANT: Snyder, Solomon H.  
 ; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric  
 ; TITLE OF INVENTION: Oxide Synthase  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Banner, Birch, McKie & Beckett  
 ; STREET: One Thomas Circle, NW  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.24  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/642.002  
 ; FILING DATE: 19910118  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kagan, Sarah A.  
 ; REGISTRATION NUMBER: 32,141  
 ; REFERENCE/DOCKET NUMBER: 1107.033576  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 296-5560  
 ; TELEFAX: (202) 296-7830  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1429 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-07-642-002-2

Query Match 12.4%; Score 678; DB 1; Length 1429;  
 Best Local Similarity 28.2%; Pred. No. 2.6e-50;  
 Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;

QY 457 GIPSPSTEQSAKKVKKAE-----NAHNTPLVLVYGSNMGTAEGTARDLADIA 504  
 Db 718 GTNGTPTKRAIGFKLAFAVFSKLMGQAMAKKVKATILYATETGSKQAVAKTLCEIF 777  
 QY 505 MSKGFAPQVALDHSAGLPRREGAVLITYASY-NCHPPDNMKQF-----547  
 Db 778 KHAFDKAMSMEEYDVLHLEHALVLTSTFGNGDPENGEKFGCALMEMRHPNSVOEE 837

QY 548 -----VDMLDQ--ASADEVKGVYSVFCGDKMATTYQKVP 582  
 Db 838 RKSXYKRFNSVSSYSDSRKSSGDPDLRDNFEETGTPLANVRFSVFLGSR-----AVPHFC 893  
 QY 583 AF--IDETLAAGAENIADRGPADSDDEFTGYEEMREHMSDVAAYFNL--DIENSED 637  
 Db 894 AFGHAVDTLLEELGGERILMRGDELCQGEAFRTWAKVFAACDVFCVGDVNIKRP 953  
 QY 638 NKSTLS-----LQFVDSADMP--LAQMH--CAFSTVNVASKELOPGSASRSTR 682  
 Db 954 NNSLISDRSKWKPKRFLTYVAEPDLTQGLSNVHKRSANRLSKHQLQSPFSRSTI 1013  
 QY 683 HLEIEL--PREASVQEGDHLGVIPIRVYEGIVNVTARF--GLDASQOIRLEAEKLAHL 738  
 Db 1014 FVRLHTNGNELQYQPDHGVFPGNHEDLVNLIIELEDAAPPANVYVKYEMLEERNAL 1073  
 QY 739 PLAKTVSVEELL-----QYVELQDPVTRTQLRANAAKTVCPRHVLEALLE-KQ 787  
 Db 1074 GVISNMKDESRLLPCTTFQAFKYVLDITTPPTPLQLOQFASLATNEKORLLVLSKGLQ 1133  
 QY 788 AYKEQVLAKRLTLELEKYPACEMKFSERIALPSIRPYVSISSSPVDEKQASTIVS 847  
 Db 1134 EYEWKKGKPTVWELEEFPSIQMPATLLTQLSLQPRYVSISSPDVYPRDEVHLTVA 1193  
 QY 848 VVSGEAMSGYGE-YKGIASNYLAELQEGDITTCFISTPOSEFTLPKDPETPLIMVPGTG 906  
 Db 1194 IVSYHTPDGEGPVNHGVCSWLMRIQADVPCFVNGAPS-FILPRNPQPCILVVGRTG 1252  
 QY 907 VAPFRGVQARK-QLKEQGOSLGEAHLVFCGRPHEDYLYQELLENANOSGII-TLHTAF 964  
 Db 1253 IAPFRSFWQOROPDIQHKGNPCPMVLVFCRCROSKI DHIYREBTLQAKNGVRELYTAY 1312  
 QY 965 SRMPNOPTKYVQVYMEDQKLI--ELLDGAFYICGDSQMAVAEATLMKSYADVHQ 1022  
 Db 1313 SREPDPRKXYVDVLQGLAESYRALKEQGGHIVCGDVTMAADVUKA-IQRLIMQOGK 1371  
 QY 1023 VSEADARLMLQOLEKGRYAKDVW 1046  
 Db 1372 LSEEDAGVFISRLRDNRRYHEDIF 1395

## RESULT 3

US-08-365-486A-13  
 ; Sequence 13, Application US/08365486A  
 ; Patent No. 5634306  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Webster, Keith A.  
 ; APPLICANT: Bishopric, Nanette H.  
 ; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
 ; TITLE OF INVENTION: Therapeutic Constructs  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dehlinger & Associates  
 ; STREET: 350 Cambridge Avenue, Suite 250  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94306  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/365.486A  
 ; FILING DATE: 23-DEC-1994  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sholtz, Charles K.  
 ; REGISTRATION NUMBER: 38,615  
 ; REFERENCE/DOCKET NUMBER: 8255-0018  
 ; TELECOMMUNICATION INFORMATION:



TELEPHONE: (415) 324-0880  
 TELEFAX: (415) 324-0960  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1429 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-365-486A-13

Query Match 12.4%; Score 678; DB 2; Length 1429;  
 Best Local Similarity 28.2%; Pred. No. 2,6e-50;  
 Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;

457 GIPSPSTEQSAKKVRKAE-----NAHNTPLVLVYGSNNGTAGTARDLADIA 504  
 DB 718 GTNGTPTKRRALGFKTLAEVKSASAKMGOMAKRVKATILVATETGKSQAVAKTCEIF 777  
 QY 505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKOF-----547  
 DB 778 KAFADAKAMSEYDIIVLHEHALVIVTSTFGNGDPPENGEKGALMEMRHPNSVOEE 837  
 QY 548 -----VDMLDQ-ASADEVKGVRYSVFGCGDKMATTYQKVP 582  
 DB 838 RKSXYKRFNSVSSYSDSRSKSSGDPDLRDNFESTGTLANVRFSVFGIGSR----AYPHFC 893  
 QY 583 AF---IDETLAAGAENIADRGEDASDDEGTYEERHEHMSDVAAVFNL--DIENSED 637  
 DB 894 AFQHAVDTLLEELGSRILKMRGDELCOGEAFRTWAKVFAACDVCVGDVNIKRP 953  
 QY 638 NKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELQCGSARSTR 682  
 DB 954 NNSLIANDSKWKNNKFRITVVAEAPDLTQGLSNVHKRVSAARLSQNLQSKFRSTI 1013  
 QY 683 HLEIEL--PREASYOGSDHLGVIPRYVEGIVNRVTARF--GLDASQOIRLEAEKLAHL 738  
 DB 1014 FVRLHTNGOEOLOYOGDHLGVFPNGHEDLVNALIERLEDAPRANHVVKEMLEERTAL 1073  
 QY 739 PLAKTVSVEELL-----QYVELQDPVTRTOLRAMAAKVCPPHKVELEALLE-KQ 787  
 DB 1074 GVISNWKDSRLPPCTIFQAFKYLLDTITPTPLQLOQFASLATNEKEKORLVLVLSGLQ 1133  
 QY 788 AYKEQVLAIRLTMLELEKYPACEMKFSERIALLPISIRPVYSSISSPRVDEKQASITVS 847  
 DB 1134 EYEEWMKGNKPTMVELEEFPSIQMPATLILLTQLSLQPRYVSISSSPDMYPRDEVHLTVA 1193  
 QY 848 VVSGEAMSGYGE-YKGIASNYLAELQEGDTITCFISTPOSEFTLPDPETPLIMVGPCTG 906  
 DB 1194 IVSYHTRDEGQPVHGVCSMILNRIQADVVPFCVFGAPRS-FILPRNPQVPCILVGPCTG 1252  
 QY 907 VAPFRFVQARK-QLEKQGSLSAEHLHYEGCRSPHEDYLKQELLENAGSGII-TLHTAF 964  
 DB 1253 IAFRFSFWOQRQDIDHKGNPCPMVLVFGCRQSKIDHIREETLQAKNGVFRRELYTAY 1312  
 QY 965 SRMPNPKTYVQVHMEODGKKLI--ELLDOGAHFYIGDGSOMAPAVEATLMSYADVHQ 1022  
 DB 1313 SRPDPKPKTYVQVLOQLAEASYRALKEGGHIIYCGDVTMAADVILKA-IQRIHQOGK 1371  
 QY 1023 VSEADARLMLQOLEKGRVAKDVM 1046  
 DB 1372 LSEEDAGVFISRLRDNRYHEDIF 1395

RESULT 4  
 US-08-319-866-11

Sequence 11, Application US/08319866  
 Patent No. 5929223

GENERAL INFORMATION:

APPLICANT: Tully, Timothy P.

APPLICANT: Yim, Jerry C.

APPLICANT: Regulski, Michael

TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES

TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY

NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02173  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/319,866  
 FILING DATE: 7-OCT-1994  
 CLASSIFICATION: 514  
 PRIOR APPLICATION NUMBER:  
 APPLICATION DATA:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Granahan, Patricia  
 REGISTRATION NUMBER: 32,227  
 REFERENCE/DOCKET NUMBER: CSHL94-03  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 861-9540  
 TELEFAX: (617) 861-9540  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1429 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-319-866-11

Query Match 12.4%; Score 678; DB 2; Length 1429;  
 Best Local Similarity 28.2%; Pred. No. 2,6e-50;  
 Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;

457 GIPSPSTEQSAKKVRKAE-----NAHNTPLVLVYGSNNGTAGTARDLADIA 504  
 DB 718 GTNGTPTKRRALGFKTLAEVKSASAKMGOMAKRVKATILVATETGKSQAVAKTCEIF 777  
 QY 505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKOF-----547  
 DB 778 KAFADAKAMSEYDIIVLHEHALVIVTSTFGNGDPPENGEKGALMEMRHPNSVOEE 837  
 QY 548 -----VDMLDQ-ASADEVKGVRYSVFGCGDKMATTYQKVP 582  
 DB 838 RKSXYKRFNSVSSYSDSRSKSSGDPDLRDNFESTGTLANVRFSVFGIGSR----AYPHFC 893  
 QY 583 AF---IDETLAAGAENIADRGEDASDDEGTYEERHEHMSDVAAVFNL--DIENSED 637  
 DB 894 AFQHAVDTLLEELGSRILKMRGDELCOGEAFRTWAKVFAACDVCVGDVNIKRP 953  
 QY 638 NKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELQCGSARSTR 682  
 DB 954 NNSLIANDSKWKNNKFRITVVAEAPDLTQGLSNVHKRVSAARLSQNLQSKFRSTI 1013  
 QY 683 HLEIEL--PREASYOGSDHLGVIPRYVEGIVNRVTARF--GLDASQOIRLEAEKLAHL 738  
 DB 1014 FVRLHTNGOEOLOYOGDHLGVFPNGHEDLVNALIERLEDAPRANHVVKEMLEERTAL 1073  
 QY 739 PLAKTVSVEELL-----QYVELQDPVTRTOLRAMAAKVCPPHKVELEALLE-KQ 787  
 DB 1074 GVISNWKDSRLPPCTIFQAFKYLLDTITPTPLQLOQFASLATNEKEKORLVLVLSGLQ 1133  
 QY 788 AYKEQVLAIRLTMLELEKYPACEMKFSERIALLPISIRPVYSSISSPRVDEKQASITVS 847  
 DB 1134 EYEEWMKGNKPTMVELEEFPSIQMPATLILLTQLSLQPRYVSISSSPDMYPRDEVHLTVA 1193  
 QY 848 VVSGEAMSGYGE-YKGIASNYLAELQEGDTITCFISTPOSEFTLPDPETPLIMVGPCTG 906

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Db      1194 IVSYHTRDGEGRVPHNGVSSWLNRIQADDDVPCFVRGAPS-FHLPBPQVPCILVPGTGT 1252
Qy      907 VAPRPGVQARK-QLKQSGSLGEAHLYFGCRSPHEHYLYOELENNOSGII-TLHTAF 964
Db      1253 IAPRSTWQOQOFDIOHKGMPCPMVLVFCGRSKIDHIREETLOAKNGVRELTYAT 1312
Qy      965 SRMPNPKTYVQVHMEODGKKLI--ELLDGAFHYICGDSGOMAPAVEATLMKSYADVHQ 1022
Db      1313 SREDRKRYVQVQVLOQLAESYRALKEQGHYVCGDVTMAADVKA-IQRIMTQOGK 1371
Qy      1023 VSEADARLWLOQLEEKGRYAKDV 1046
Db      1372 LSEEDAGVFISRLRDNRYHEDIF 1395

RESULT 5
US-08-880-342-13
Sequence 13, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Shultz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1429 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-880-342-13

Query Match 12.4%; Score 678; DB 4; Length 1429;
Best Local Similarity 28.2%; Pred. No. 2.6e-50;
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;
Qy      457 GIPSPSTEQSAKKYRKAE-----NANTPLLVYGSNMGAESTADLADIA 504
Db      718 GTNGTPTKRRRAIGFKLAEAVFSAKJMGOMAKRVKATILYATETGKSQAVATLCEIF 777

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Qy      505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPDPNAKOF----- 547
Db      778 KHAFFDAKAMMEYDYLVHLEHALVLTSTFGNQPPENGEFGALMEMRHPNSVOEE 837
Qy      548 -----VMDLO-ASADEKGYRVSFGCGDNMATTYQKVP 562
Db      838 RKSYKRVENSVSYSRKSCKGDPDLRDNFESTGPLANRVFVFGISR----AYPHFC 893
Qy      583 AF---IDETLAAGANINADRGADASDDPEGYEEMREHMWDVAAYFL--DIENSED 637
Db      894 AFGHAVDTLLEELGGERILKMRGDELCOGEAFRTWAKVFAACDVFCVGDVINIKP 953
Qy      638 NKSTLS-----LQFVDSAADMP--LAKCH--GAFSTNVVASKELOQPGASASTR 682
Db      954 NNSLISNDKRWKRNKRLTYVAEAPDLTQGLSNVHKRVSAAALLRQUNQSPKFSSTI 1013
Qy      683 HLEIEL--PREASYQEGDHLGVIPRNYEGIVNVTARF--GLDASQOIRLEAEKLAHL 738
Db      1014 FVRLHTNGNQLQYQGDHLGVFPGNHEDLVNALLERLEDPAPPANHVVKVEMLEERTAL 1073
Qy      739 PLAKTVSEELL-----QYVELQDPVTRTOLRAMAKTVCPHKELEALLE-KQ 787
Db      1074 GVISMWKBESRLPCTTFQAFKYLLDTTPPTPLQOQFASLATNEKEKORLVLVSKGLQ 1133
Qy      788 AYEQVLAKRLTMLLELEKYPACEMKSFERIALLPISIRPVYSSISSPRYDEKQASITVS 847
Db      1134 EYEMKMKGNKPTVNEVLEERSIQMPATILLTQLSLQPPRYSSISSPRYDEKQASITVS 1193
Qy      848 VSGEAMSGYGE-YKGIASNYLAELQEGDTTTFISTPOSEFTLPDOPETPLIMVGBTG 906
Db      1194 IVSYHTRDGEGRVPHNGVSSWLNRIQADDDVPCFVRGAPS-FHLPBPQVPCILVPGTGT 1252
Qy      907 VAPRPGVQARK-QLKQSGSLGEAHLYFGCRSPHEHYLYOELENNOSGII-TLHTAF 964
Db      1253 IAPRSTWQOQOFDIOHKGMPCPMVLVFCGRSKIDHIREETLOAKNGVRELTYAT 1312
Qy      965 SRMPNPKTYVQVHMEODGKKLI--ELLDGAFHYICGDSGOMAPAVEATLMKSYADVHQ 1022
Db      1313 SREDRKRYVQVQVLOQLAESYRALKEQGHYVCGDVTMAADVKA-IQRIMTQOGK 1371
Qy      1023 VSEADARLWLOQLEEKGRYAKDV 1046
Db      1372 LSEEDAGVFISRLRDNRYHEDIF 1395

RESULT 6
US-08-705-625-4
Sequence 4, Application US/08705625
Patent No. 5908756
GENERAL INFORMATION:
APPLICANT: Snyder, Solomon H.
APPLICANT: Jaffrey, Samie R.
TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,625
FILING DATE: 30-AUG-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.

```



QY 739 PLAKTVSVEELL-----QYVELODPVTRTOLRAMAKTVCPPHKVELEALLB-KQ 787  
Db 1074 GVISNMKDESRLEPPTIFQAFKYYLIDITPTPTLOQGFASLANEKKRLVLVLSGLQ 1133  
QY 788 AYKQVLAKRLTLMLEKYPACEMKSEEFALLPSIRPRYYSISSSPRVDEKQASTVS 847  
Db 1134 EYEWKMGKKNPTWVELEEPSIQMPAPLLTOLSLQPRYYSISSSPDMVPDEVHLTVA 1193  
QY 848 VVSGEAMSGYGE-XKGIASNYLAELOEGDITTCFISTQSEFTLPKDEPTLIMVPGTG 906  
Db 1194 IVSHTHDEGEPVHGVSSMLNRIQADVPVPCVGRAPS-FHLPRNQVPCILVGPETG 1252  
QY 907 VAPRGFVQARK-OLKEQGOSLGEANLYFGCRSPHEDYLYOELENAOSEGII-TLHTAF 964  
Db 1253 IAPRPSFWQORQFDIOHKGNPCPMVLVFGCRQSKIDHIREETLQAKNGVPRELYTAY 1312  
QY 965 SRMNPQRTYVOHVMEDQDKLI--ELLDOGAHFYICGDSQMAPAVEATLMKSYADVHQ 1022  
Db 1313 SREBDRPKKYVDVLOQLAESYRALKEQGHIYVCGDVTMAADVLA-KA-IQIMTQOGK 1371  
QY 1023 VSEADARLMLQOLEEKGKRYAKDV 1046  
Db 1372 LSEEDAGVFISRLDNRHYHEDIF 1395

## RESULT 8

US-09-220-574-4  
Sequence 4, Application US/09220574  
Patent No. 6168926

## GENERAL INFORMATION:

APPLICANT: Snyder, Solomon H.  
APPLICANT: Jaffrey, Samie R.  
TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Witcoff  
STREET: 1001 G Street, N.W.  
CITY: Washington, D.C.  
COUNTRY: U.S.A.  
ZIP: 20001-4597  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/220,574  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/705,625  
FILING DATE: 30-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107,57071  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1430 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-220-574-4

Query Match 12.4%; Score 678; DB 4; Length 1430;  
Best Local Similarity 28.2%; Pred. No. 2,6e-50;

Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;  
QY 457 GISPSTEQSAAKVRKAE-----NAHNPLVLVYSGNMGTAGTRADLADIA 504  
Db 718 GINGTPTKRAIGFKLAIEVKSAKIMGQAMKRVKATILLVITETGSKQAYAKTLCEIF 777  
QY 505 MSKFAFQVATLDSHAGNLPRGAVLIVTASY-NGHPDNKAF----- 547  
Db 778 KHAFDAKAMEEYDIHLEHALVLVSTFGNGDPPENGEKGALMEMRHPNSVOEE 837  
QY 548 -----VMDLQ-ASADEVKGRYVFGGDKMATTYKVP 582  
Db 838 RKSXYKAFNSVSSYSDSRKSGDGPDLRDNFBESTGPLANRVFSVFGIGSR---AYPHFC 893  
QY 583 AF---IDETLAAGAENIADRGADSDDEGTYEERBEMHMSDVAYFUL--DIENSED 637  
Db 894 AFGHAUTLLEELIGENILKMRGDELGGEEAFRTAKVFFAACDVFVGDDVNIKP 953  
QY 638 NKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELQPGSARSTR 682  
Db 954 NNSLISNDKSMKKNKFRLYVAEAPDLTGLSNVHKRVGABRLSRQNLQSPKSRSTI 1013  
QY 683 HLEIEL--PKFASYQSDHIGVIRNYEGIVNRYTARF--GLASQOIRLEABEKLALH 738  
Db 1014 FVRLHTNGNOELOYPGDHLGVFPGNHEDLVNALIERLEDAPAPNHVVKEMLEERTAL 1073  
QY 739 PLAKTVSVEELL-----QYVELODPVTRTOLRAMAKTVCPPHKVELEALLB-KQ 787  
Db 1074 GVISNMKDESRLEPPTIFQAFKYYLIDITPTPTLOQGFASLANEKKRLVLVLSGLQ 1133  
QY 788 AYKQVLAKRLTLMLEKYPACEMKSEEFALLPSIRPRYYSISSSPRVDEKQASTVS 847  
Db 1134 EYEWKMGKKNPTWVELEEPSIQMPATLLTQSLQPRYYSISSSPDMVPDEVHLTVA 1193  
QY 848 VVSGEAMSGYGE-XKGIASNYLAELOEGDITTCFISTQSEFTLPKDEPTLIMVPGTG 906  
Db 1194 IVSHTHDEGEPVHGVSSMLNRIQADVPVPCVGRAPS-FHLPRNQVPCILVGPETG 1252  
QY 907 VAPRGFVQARK-OLKEQGOSLGEANLYFGCRSPHEDYLYOELENAOSEGII-TLHTAF 964  
Db 1253 IAPRPSFWQORQFDIOHKGNPCPMVLVFGCRQSKIDHIREETLQAKNGVPRELYTAY 1312  
QY 965 SRMNPQRTYVOHVMEDQDKLI--ELLDOGAHFYICGDSQMAPAVEATLMKSYADVHQ 1022  
Db 1313 SREBDRPKKYVDVLOQLAESYRALKEQGHIYVCGDVTMAADVLA-KA-IQIMTQOGK 1371  
QY 1023 VSEADARLMLQOLEEKGKRYAKDV 1046  
Db 1372 LSEEDAGVFISRLDNRHYHEDIF 1395

## RESULT 9

US-08-365-486A-21

Sequence 21, Application US/08365486A  
Patent No. 5834306

## GENERAL INFORMATION:

APPLICANT: Webster, Keith A.  
APPLICANT: Bishopric, Nanette H.  
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
;   NAME: Sholtz, Charles K.
;   REGISTRATION NUMBER: 38,615
;   REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 324-0880
;   TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1433 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-365-486A-21

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Query Match 12.4%; Score 675; DB 2; Length 1433;

Best Local Similarity 28.0%; Pred. No. 4.9e-50;

Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

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QY 457 GIPSPTEGSAKVRKKA-----NAHNPFLVLYGSMNGTAGTARDLADIA 504
DB 722 GTNGTPTKRRALGFKKLAEVKSAKLMGQAMAKRVKATLLVATETGSAQVAKTICEI- 780
QY 505 MSKGPAQVATLDH-AGNLPREGAVLITASY-NGHPDPAKOF-----547
DB 781 FKIAFDKAVMSMEYDIYVHLEHETLVLVSTGNDPPENGKFGCALMEMHPSVQE 840
QY 548 -----VDWLDQ-ASADEVKGVRYSVFSGCDKNMATTYQKV 581
DB 841 ERKSYKRVNSVSSYSDSQSGDGPDLRNFESAGPLANVRSPVGLGSR-----AYPHF 896
QY 582 PAF---IDETLAKGAENIADRGADASDPEFTYEEMKHMSDVAAYNLT--DIENSE 636
DB 897 CAGHADVTLLELGEERILKMEGDELCGQEAFTMAKVFKAACDVCVGDVNIK 956
QY 637 DNKSTLS-----LOFVDSADMP--LAKMH--GAFSTNVVASKELQOGSARST 681
DB 957 ANNSLSLNDBSMKRKNFRLTFVAEAPLTOGLSNVHKRVSAARLISRONLQSPKSRST 1016
QY 682 RHLEIEL--PKEASVQEGDHLGVIPRNYEGIVNRVTARFGIDA---SQQIRLEAEERK-- 734
DB 1017 IFVRLHTNGSQELQYQPGDHLGVFPGNHEDLVNALIERLE-DAPVNVQWKVELLEBRNT 1075
QY 735 -----LAHLPLAKTVSEELLQYVELQDPVTRTQLRAMAAKTVCPHKVLEALLE- 785
DB 1076 ALGVISNMTDELRLPCTIFQAFKYULDTTPPTPLQLOQFASLATSSEKORLLVLSKG 1135
QY 786 KQAYKQOVLAKRLTMTLELEKYPACEMKSEFIALPSIRPRYSSISSSPRVDEKQASIT 845
DB 1136 LQYIEEMKMKNPITYEVLFEFPIQMPATLLTQLSLQOPRYSSISSSDMPDPDEVHLT 1195
QY 846 VSVVSGEAMSGYGE-YKGIASNYLAELQEGDITTCFISTPOSEFTLPKDEPFLINWPG 904
DB 1196 VALVSVTRTRGEGEPIHHGVCSWLNRIQADELVPCFVRGAPF-FHLPBRNQVPCILVPG 1254
QY 905 TGVAPFRGVOQARK-OLKEQOGLGEAHLYFGCRSHEDVLYOELENAOSEGII--TLHT 962
DB 1255 TGIAPFRSFQOQRFDIQHGKMPCPMVLVFGCRSQSKIHIYREETLQAKNGKVFRELYT 1314
QY 963 AFSRMPNQPTVYQVHWEDQGGKLL--ELLDQGANFYICGDSGQMAPAVATLTKSYADV 1020
DB 1315 AYREBPDKRKYVODILOEQDLASVYRALKEQGGHIVYCGDVTMAADVLA-KA-IQRIMTQ 1373
QY 1021 HOVSEADARLMLQOLEEKGRYAKDV 1046
DB 1374 GKLSAEDAGVFISMARDNRYHEDIF 1399

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RESULT 10

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US-09-123-708-4
; Sequence 4, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Uergen
; APPLICANT: GORDECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; FILE REFERENCE: 51169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1433
; TYPE: PRT
; ORGANISM: Cytomegalovirus
; US-09-123-708-4

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Query Match 12.4%; Score 675; DB 4; Length 1433;

Best Local Similarity 28.0%; Pred. No. 4.9e-50;

Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

```

QY 457 GIPSPTEGSAKVRKKA-----NAHNPFLVLYGSMNGTAGTARDLADIA 504
DB 722 GTNGTPTKRRALGFKKLAEVKSAKLMGQAMAKRVKATLLVATETGSAQVAKTICEI- 780
QY 505 MSKGPAQVATLDH-AGNLPREGAVLITASY-NGHPDPAKOF-----547
DB 781 FKIAFDKAVMSMEYDIYVHLEHETLVLVSTGNDPPENGKFGCALMEMHPSVQE 840
QY 548 -----VDWLDQ-ASADEVKGVRYSVFSGCDKNMATTYQKV 581
DB 841 ERKSYKRVNSVSSYSDSQSGDGPDLRNFESAGPLANVRSPVGLGSR-----AYPHF 896
QY 582 PAF---IDETLAKGAENIADRGADASDPEFTYEEMKHMSDVAAYNLT--DIENSE 636
DB 897 CAGHADVTLLELGEERILKMEGDELCGQEAFTMAKVFKAACDVCVGDVNIK 956
QY 637 DNKSTLS-----LOFVDSADMP--LAKMH--GAFSTNVVASKELQOGSARST 681
DB 957 ANNSLSLNDBSMKRKNFRLTFVAEAPLTOGLSNVHKRVSAARLISRONLQSPKSRST 1016
QY 682 RHLEIEL--PKEASVQEGDHLGVIPRNYEGIVNRVTARFGIDA---SQQIRLEAEERK-- 734
DB 1017 IFVRLHTNGSQELQYQPGDHLGVFPGNHEDLVNALIERLE-DAPVNVQWKVELLEBRNT 1075
QY 735 -----LAHLPLAKTVSEELLQYVELQDPVTRTQLRAMAAKTVCPHKVLEALLE- 785
DB 1076 ALGVISNMTDELRLPCTIFQAFKYULDTTPPTPLQLOQFASLATSSEKORLLVLSKG 1135
QY 786 KQAYKQOVLAKRLTMTLELEKYPACEMKSEFIALPSIRPRYSSISSSPRVDEKQASIT 845
DB 1136 LQYIEEMKMKNPITYEVLFEFPIQMPATLLTQLSLQOPRYSSISSSDMPDPDEVHLT 1195
QY 846 VSVVSGEAMSGYGE-YKGIASNYLAELQEGDITTCFISTPOSEFTLPKDEPFLINWPG 904
DB 1196 VALVSVTRTRGEGEPIHHGVCSWLNRIQADELVPCFVRGAPF-FHLPBRNQVPCILVPG 1254
QY 905 TGVAPFRGVOQARK-OLKEQOGLGEAHLYFGCRSHEDVLYOELENAOSEGII--TLHT 962
DB 1255 TGIAPFRSFQOQRFDIQHGKMPCPMVLVFGCRSQSKIHIYREETLQAKNGKVFRELYT 1314
QY 963 AFSRMPNQPTVYQVHWEDQGGKLL--ELLDQGANFYICGDSGQMAPAVATLTKSYADV 1020
DB 1315 AYREBPDKRKYVODILOEQDLASVYRALKEQGGHIVYCGDVTMAADVLA-KA-IQRIMTQ 1373
QY 1021 HOVSEADARLMLQOLEEKGRYAKDV 1046

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Db      1374 GKLSAEDAGVFISRMDDNRYHEDIF 1399

RESULT 11
US-09-123-624-4
Sequence 4, Application US/09123624
Patent No. 6149936
GENERAL INFORMATION:
APPLICANT: SCHRAEDER, Jurgen
APPLICANT: CODECKER, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
FILE REFERENCE: 51169-2004
CURRENT APPLICATION NUMBER: US/09/123,624
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 08/553,503
PRIOR FILING DATE: 1996-03-01
PRIOR APPLICATION NUMBER: 441402.8
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 1433
TYPE: FRT
ORGANISM: Homo sapiens
US-09-123-624-4

Query March      12.4% Score 675; DB 4; Length 1433;
Best Local Similarity 28.0%; Pred. No. 4.9e-50;
Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

Cy      457 GIPSPSTEOSAKVKRKAE-----NANHTPLVLVYGSNMGTAGTARDLADIA 504
Db      722 GTNGTPTKRRAIGKRLAEAVKFSAKLMGQAMAKRVKATILVATETGSAQVAKTLCET 760
Cy      505 MSKGFAPQVATLDSH-AGNLPREGAVLITVASY-NGHPPDNAKOF-----547
Db      781 FKHAFDKVMSEBYDIVHLEHETLVLVVSTFGNGDPENGEKFGCALMEMRHPNSVOE 840
Cy      548 -----VMDLQD-ASADEVKVRSYVFGCGDKNATTYQKV 581
Db      841 ERKSYKVRNSVSSYSQSKSGGDPDLRDNFESAGFLANVRSFVGLGSR---AYPHF 896
Cy      582 PAF--IDETLAAGAENIADRGDASDDEGTVEEREMHMSDVAAFMU--DIENSE 636
Db      897 CAFGHAVDTLLELGERIILKMRGDELCGGBAFAKVFRAACVFCVGDVNIEX 956
Cy      637 DNKATLS-----LQVDSADMP--LAKKH-GAFSTNVVASKELQQGASRST 681
Db      957 ANNSLISNDRSMKRNKFRLTVAEAPBLTQGLSNVHKRVSAAARLLSRQNSPKSRST 1016
Cy      682 RHLLELU--PKKASYOEGDHLGVI PRNVEGIVNRYTARFGDA---SQQIRLEAEEK-- 734
Db      1017 IFVRLHTNGSOELOQOPGDHLGVFPNGHEDLVNAILERLE-DAPPVNMVAVELLEENT 1075
Cy      735 -----LAHLPLAKTVSEELLQYVELQDPVTRTQLRAMAAKTVCPPHKELEALLE- 785
Db      1076 ALGVISMTWDELRLPPTCTFOAFKXYLDITTPRPLQLOQFASLASEKQRLLVLVSKG 1135
Cy      786 KQAYKEOVLAKRLIMLELLEKYPACEMKFSFIALPSIRRYYSISSSPRYDEKOSIT 845
Db      1136 LQEEYEMKMGKNPITVELEEFPSIQMPATLLTLQSLQPRYYSSISSPMYDEVALT 1195
Cy      846 VSVVSGEAMSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGRG 904
Db      1196 VAISYRTRDEGPIRHGVCSSWLNRIADAVLPFCVAGAPS-FLHPNPQVPCILVGPBG 1254
Cy      905 TGVA PRFGVQARK-QLKEGOSLGEAHLVFCGRSPHEDYLVOBELENAQSEGII--TLAT 962
Db      1255 TGIA PRFSFWQORQDIOHKGMNPPMWLVFCGCRQSKIDHLYRETTLOAKKXGFRRELYT 1314
Cy      963 AFSGMNPQKTYIVQHWEOQDKKLI--ELLQGAHFYICGPGSQMAPVAVETLMAKSTADV 1020

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Db      1315 AYSRHPDPKKYVODILOEQBLAESVYRALKEOGGHIVYCGDVTMAADVLKA-IQRIWTOQ 1373
Cy      1021 HOVSADARLMLQOLEKEGRYAKDWM 1046
Db      1374 GKLSAEDAGVFISRMDDNRYHEDIF 1399

RESULT 12
US-08-880-342-21
Sequence 21, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: Delinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1433 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-880-342-21

Query March      12.4% Score 675; DB 4; Length 1433;
Best Local Similarity 28.0%; Pred. No. 4.9e-50;
Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

Cy      457 GIPSPSTEOSAKVKRKAE-----NANHTPLVLVYGSNMGTAGTARDLADIA 504
Db      722 GTNGTPTKRRAIGKRLAEAVKFSAKLMGQAMAKRVKATILVATETGSAQVAKTLCET 760
Cy      505 MSKGFAPQVATLDSH-AGNLPREGAVLITVASY-NGHPPDNAKOF-----547
Db      781 FKHAFDKVMSEBYDIVHLEHETLVLVVSTFGNGDPENGEKFGCALMEMRHPNSVOE 840
Cy      548 -----VMDLQD-ASADEVKVRSYVFGCGDKNATTYQKV 581
Db      841 ERKSYKVRNSVSSYSQSKSGGDPDLRDNFESAGFLANVRSFVGLGSR---AYPHF 896

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QY 582 PAR---IDETLAKGAENIADRGADASDDEGTYEEMRHMMSDVAAYNUL--DIENSE 636
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DB 897 CARGHADVTLLEELGGERILKMRGDELCSGEBAFRTWAKVFAACDVFCVGDVNIIEK 956
| | | | |
QY 637 DNKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELQOGSARST 681
| | | | |
DB 957 ANNSLSINDRSMWKNKFRLLTFVABAPBLTQGLSNVHKRVSAARLSRONLOSPKSRST 1016
| | | | |
QY 682 RHEIEL--PKEASVOEGDHLGVI PRYEGIVNVTARFGLDA---SQOIRLEAEEK-- 734
| | | | |
DB 1017 IFRRLHTNGSOELOYOQGDHGVFPNGHEDLVNALIERLE-DAPPVQWAKVELLEERN 1075
| | | | |
QY 735 -----LAHLPLAKTVSVEELLQYVELODPVTROTQRAMAAKTVCPPHKEVLEALLE- 785
| | | | |
DB 1076 ALGVISNMTDELRLPCTTIFQAFKYLDITTPPTPLQLOQFASLATSSEKORLLVLSKG 1135
| | | | |
QY 786 KOAYKEQVLAKRLTMLLEKYPACEMKFSEFIALLSIRPRYVSISSSPRVDEKQASIT 845
| | | | |
DB 1136 LOEYEEKWKGNKPTIVLEFPESIQMPATLLTQLSLQPRYVSISSSPDMVDEVHLT 1195
| | | | |
QY 846 VSVVSGEAMSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDETPLIWVPG 904
| | | | |
DB 1196 VALVSYRTDGEPIHNGVSSWLNRIQADELVPCFVRGAPS-FHLPRNQVPCILVPG 1254
| | | | |
QY 905 TGVAPFRGFYQARK-OLKEGOSLGEAHLVFGCRSPHEDVLYOELENAQSEGIT-TLHT 962
| | | | |
DB 1255 TGLAPFRSFWOQROFDIOHKGNMPCPVVLVFGCRQSKIDHIYRETLQANKKGVFRELYT 1314
| | | | |
QY 963 AFSPMPNQPTTYQVHMEODGKLI--ELLDGAFHFCGDSQMAPAVEATLMKSYADV 1020
| | | | |
DB 1315 AYREBPKPKKYVODILOEQBLAESVYRALKEOGGHIYVCGDVTMAADVLA-10RIMTQO 1373
| | | | |
QY 1021 HOVSEADARLMOOLEBKGRYADV 1046
| | | | |
DB 1374 GKLSAEDAGVFSMRDNRHYHEDIF 1399
| | | | |

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RESULT 13
US-08-365-486A-19
; Sequence 19, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1434 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-365-486A-19

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Query Match 12.4%; Score 675; DB 2; Length 1434;
Best Local Similarity 28.0%; Pred. No. 4,9e-50;
Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

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QY 457 GIPSPTEGSAKKVRKAE-----NAHNPPLVLVYGSNNGTAGTARDLADIA 504
| | | | |
DB 723 GINGPTPKRAAICFKKLAENVKFSAKLMGQAMKRVKATLLVATETGSKQAVAKTCEI- 781
| | | | |
QY 505 MSKGPAPQVATLDSH-AGNLPREGAVILVYASV-NGHPNNAKOF----- 547
| | | | |
DB 782 FKHAFAKMSMEBYDVLVHEHTLVLVVSTGNGDPRNGKFGCALKMEMHNSVOE 841
| | | | |
QY 548 -----VDWLDQ--ASADEVKGRVSVFGCGDKMATTYQKV 581
| | | | |
DB 842 ERKSYKVRFNVSASYSQSGSDGPDRLRNFESAGPLANVRFSVFGIGSR---AYPHF 897
| | | | |
QY 582 PAR---IDETLAKGAENIADRGADASDDEGTYEEMRHMMSDVAAYNUL--DIENSE 636
| | | | |
DB 898 CARGHADVTLLEELGGERILKMRGDELCSGEBAFRTWAKVFAACDVFCVGDVNIIEK 957
| | | | |
QY 637 DNKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELQOGSARST 681
| | | | |
DB 958 ANNSLSINDRSMWKNKFRLLTFVABAPBLTQGLSNVHKRVSAARLSRONLOSPKSRST 1017
| | | | |
QY 682 RHEIEL--PKEASVOEGDHLGVI PRYEGIVNVTARFGLDA---SQOIRLEAEEK-- 734
| | | | |
DB 1018 IFRRLHTNGSOELOYOQGDHGVFPNGHEDLVNALIERLE-DAPPVQWAKVELLEERN 1076
| | | | |
QY 735 -----LAHLPLAKTVSVEELLQYVELODPVTROTQRAMAAKTVCPPHKEVLEALLE- 785
| | | | |
DB 1077 ALGVISNMTDELRLPCTTIFQAFKYLDITTPPTPLQLOQFASLATSSEKORLLVLSKG 1136
| | | | |
QY 786 KOAYKEQVLAKRLTMLLEKYPACEMKFSEFIALLSIRPRYVSISSSPRVDEKQASIT 845
| | | | |
DB 1137 LOEYEEKWKGNKPTIVLEFPESIQMPATLLTQLSLQPRYVSISSSPDMVDEVHLT 1196
| | | | |
QY 846 VSVVSGEAMSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDETPLIWVPG 904
| | | | |
DB 1197 VALVSYRTDGEPIHNGVSSWLNRIQADELVPCFVRGAPS-FHLPRNQVPCILVPG 1255
| | | | |
QY 905 TGVAPFRGFYQARK-OLKEGOSLGEAHLVFGCRSPHEDVLYOELENAQSEGIT-TLHT 962
| | | | |
DB 1256 TGLAPFRSFWOQROFDIOHKGNMPCPVVLVFGCRQSKIDHIYRETLQANKKGVFRELYT 1315
| | | | |
QY 963 AFSPMPNQPTTYQVHMEODGKLI--ELLDGAFHFCGDSQMAPAVEATLMKSYADV 1020
| | | | |
DB 1316 AYREBPKPKKYVODILOEQBLAESVYRALKEOGGHIYVCGDVTMAADVLA-10RIMTQO 1374
| | | | |
QY 1021 HOVSEADARLMOOLEBKGRYADV 1046
| | | | |
DB 1375 GKLSAEDAGVFSMRDNRHYHEDIF 1400
| | | | |

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RESULT 14
US-08-880-342-19
; Sequence 19, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Ladecroute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates

```

STREET: 350 Cambridge Avenue, Suite 250  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94306  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/880,342  
 FILING DATE: 23-JUN-1997  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PCT/IB95/00996  
 FILING DATE: 13-NOV-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/365,486  
 FILING DATE: 23-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sholtz, Charles K.  
 REGISTRATION NUMBER: 38,615  
 REFERENCE/DOCKET NUMBER: 8255-0018.30  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 324-0880  
 TELEFAX: (415) 324-0960  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1434 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-880-342-19

Query Match 12.4%; Score 675; DB 4; Length 1434;  
 Best Local Similarity 28.0%; Pred. No. 4.9e-50;  
 Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

457 GIPSPSTEOSAKKVRKAE-----NHNTPPLVLVYSGMGTAGTADLADIA 504  
 DB 723 GTNGTPTIKRAIGFKLAEAVKFSAKLMGQAMAKRVKATILVETGSKQAVKTLCEI- 781  
 QY 505 MSKGFAPQVATLDH-AGNLPRGAVLITVASY-NGHPPDNAKOF----- 547  
 DB 782 FKAFADAKVMSMEYDIVLHEHTLVLVVSTFGNGDPDPENGEKFGCALMEMRHPNSVOE 841  
 QY 548 -----VDMLDQ-ASADEVKVRYSVFGCGDKNMATTYQKV 581  
 DB 842 ERKSKYKRVNSVSSYSDQKSSGDDPDLRDNFESAGPLANVRFSVFGLSR---AYPHF 897  
 QY 582 PAF---IDETLAAGAENIADRGESADDEEGTYEEREMHMSVAAVFL--DIENSE 636  
 DB 898 CAFGHAVDTLLEJGGERILKMRBDELCGQEBARVAKVFAACDFVCGDVNIETK 957  
 QY 637 DNKSTLS-----LQFVDSADMP--LAKKH--GAFSTWVASKELQOFGSAST 681  
 DB 958 ANNGLISNDRSMKKNKRLTFVAEAPRLTQGLSNVHKRVAARLNSQNSQSPSSRST 1017  
 QY 682 RHEIEL--PKYASQESDHLGVTPRYEGVYRVTARFGDA--SQOILEAEER-- 734  
 DB 1018 IFVRLHTNGSOELOYPGDHLGVFPGNHEDVNLIERLE--DAPVNMQVVELLEERT 1076  
 QY 735 -----LAHLPLAKTVSVLELQVVELQVLPVTRTQRAMAAKTVCPRHVLEALLE- 785  
 DB 1077 ALGVISNMTDELRLPPTTFQAFKYIDITTPPTPLQOQFASLATSKEKQRLVLVSKG 1136  
 QY 786 KQAYKEQVLAQLTLLELEKYPACEMKSEFIALPSPRPVYSSISSPVDKQASIT 845  
 DB 1137 LQVBEWMWGNKPTIVLEEFPSIQMPATILLQSLQPRYSSISSPPMYPVCHLT 1196  
 QY 846 VSVVSGEAMSGYE-YKGIASNYLAELQEGDTITCFISTPOSEFTLPPDEPTPLIMVPG 904

DB 1197 VAIVSYRTDRDEGPIHHGVSSWMLNRIQADELVPCFVRGAP- FHLPRNPQVCLIVPG 1255  
 QY 905 TGVAAPRGFVQARK-OLKEQGOSLGEAHLVFGGRSPHEDVLYOEBELNAOSEGII-TLHT 962  
 DB 1256 TGIAPFRSFQOQROFQIKGMNPPCMVTLVFGKQSKIDHTIYEBETIQAKKGVFRELTY 1315  
 QY 963 AFSRMPNQPKTYQVHWMEODGKLI--ELDDQAHFYICGDSGQMAPAVEATLMKSYADV 1020  
 DB 1316 AYSREPDKPKKYQDILQEQLASVYRALKEQGGHIVYCGDVTMAADVLA-IQRIWTOQ 1374  
 QY 1021 HQVSEADARLMLQOLEKGRYADW 1046  
 DB 1375 GKLSAEDAGVIFSRMDRNRHEDIF 1400

RESULT 15  
 US-08-705-625-3  
 Sequence 3, Application US/08705625  
 Patent No. 5908756  
 GENERAL INFORMATION:  
 APPLICANT: Snyder, Solomon H.  
 TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric  
 TITLE OF INVENTION: Oxide Synthase  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Banner & Witcoff  
 STREET: 1001 G Street, N.W.  
 CITY: Washington, D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20001-4597

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/705,625  
 FILING DATE: 30-AUG-1996  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kagan, Sarah A.  
 REGISTRATION NUMBER: 32,141  
 REFERENCE/DOCKET NUMBER: 01107.57071  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-508-9100  
 TELEFAX: 202-508-9239  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1554 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Rattus norvegicus  
 US-08-705-625-3

Query Match 12.4%; Score 675; DB 2; Length 1554;  
 Best Local Similarity 28.0%; Pred. No. 5.6e-50;  
 Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

457 GIPSPSTEOSAKKVRKAE-----NHNTPPLVLVYSGMGTAGTADLADIA 504  
 DB 723 GTNGTPTIKRAIGFKLAEAVKFSAKLMGQAMAKRVKATILVETGSKQAVKTLCEI- 781  
 QY 505 MSKGFAPQVATLDH-AGNLPRGAVLITVASY-NGHPPDNAKOF----- 547  
 DB 782 FKAFADAKVMSMEYDIVLHEHTLVLVVSTFGNGDPDPENGEKFGCALMEMRHPNSVOE 841  
 QY 548 -----VDMLDQ-ASADEVKVRYSVFGCGDKNMATTYQKV 581  
 DB 842 ERKSKYKRVNSVSSYSDQKSSGDDPDLRDNFESAGPLANVRFSVFGLSR---AYPHF 897



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Db 212 LEEDFTWREQFPAVCEHFGVEATGSESSIRQYELVHTDIDAKVYMGEMGLKSYEN 271
Qy 660 -----GASFTNVVASKELQOGSARSTRHLEIL-PKEASYOEGBHLGIVIRNVEGI 710
Db 272 QKPFPAKNPFLAATTNRKLNQ-GTERHMLHLELSDSKIRYESGDHVAVPANASAL 330
Qy 711 VNRVTARFG--LDASQOIRLEAEBEKLAHLPLAKTVSEVLELQYVELQDPVTRTOLPAMA 768
Db 331 VNOGKILGADLDVVMISLNNIDESNKKHPPCTSTRALTLYLDITNF-PRINVLVEL 389
Qy 769 AKTYCPHAKVELELLE-----KQAYKEQVLAKRLTMLELEKYPACMEKSFELLAP 822
Db 390 AQVASESEOELEKRMASSGEGKELYLSWVEARRHLLALQCPFLRPIDHICELLP 449
Qy 823 SIRPRYSISSPRVDEKQASITVSVSGEAMSGVEGKIASNYL-AELOEGPT----- 876
Db 450 RLQKRYTISASSKVNHSVHICAVVEYETKAGRIN-KGATWMLRKEVGVENGGRAL 508
Qy 877 ITCFISTPOSEFTLPKDEPRLINVGPGTVAPRFGVQARKOLKEQOSLGEAHLTFGC 936
Db 509 VPMFVR--KSGFRLPFAKTFPVMVGPGTVAPRFGIQLERAWLRQGEKVEGTLVLYGC 566
Qy 937 RSPHEDLYOELENAOSEGIIT-LHTAFSMPNOPKTYVOHVMEOGDKLIELLDGAAH 995
Db 567 RRSDELYLYREELAQFHRDGLTQLNVAFSREOSH-KVYVQHLKODREHMLKLEGGAAH 625
Qy 996 FYICGDSQMAPAVEATLMSYADVHOVSEADARLMLQLEBKGRYAKDWA 1047
Db 626 IYVCGDARNMARDVONTFYDVLAEIGMEHAQAVDIKMLTKGRYSLDVAWS 677

```

## RESULT 2

```

US-09-765-873A-14
: Sequence 14, Application US/09765873A
: Patent No. US20010053847A1
: GENERAL INFORMATION:
: APPLICANT: Tang, Xiao-Song
: TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
: FILE REFERENCE: BC1009 US CIP
: CURRENT APPLICATION NUMBER: US/09/765,873A
: CURRENT FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: US 09/627,216
: PRIOR FILING DATE: 2000-07-27
: PRIOR APPLICATION NUMBER: US 60/147,719
: PRIOR FILING DATE: 1999-08-06
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 14
: LENGTH: 588
: TYPE: PRT
: ORGANISM: Helianthus tuberosus
US-09-765-873A-14

```

Query Match 12.9%; Score 705.5; DB 10; Length 588;  
 Best Local Similarity 31.9%; Pred. No. 1.8e-43;  
 Matches 189; Conservative 92; Mismatches 245; Indels 67; Gaps 19;

```

Qy 499 DLADIANSKGPAPVATLDSHAGNLPRGAVLITVASY-NGHPPDNMKQFVMDLQASAD 557
Db 18 DLDIYA-----ADDEYAEKFKKETFAPFLATYGDDEPTDNARFKWTEG-- 65
Qy 558 EVKGV-----RYSVFGCDKRMWATTYQVPAFIDETLLAKAENIADRGADASDDEFGT 612
Db 66 DDKVWLEKHYGVFGKNGKQY-EHFNKIALVNBEGULQEGAKRFVPVGLDDDDOSIEDD 124
Qy 613 YEEPRHMSDVAAYFNLDIENSDDNS-----TSL-----QVSAADMP 655
Db 125 FSAKKEIWPMLDQL-LD-----EDDKTAATPYTAALPEYRVVPHDKDPTSEHNSQTNG 179
Qy 656 AKMGA---FSTNVVASKELQOGSARSTRHLEILPKEA-SYOGDHLGIVIRNVEGI 711
Db 180 HTVDAHQPCRSNVAVKKEHLTPESDRSCHLEPDISHTGSLYETGHDVGVYCNLIEVV 239

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Qy 712 NRYTARFGLDASQOIRLEAEBEKLAHL-----PLAKTVSEVLELQYVELQDPVTRTOL 764
Db 240 EEAEXKILGLPADYVPSLHIDNEDGTPLGPTLPPEPPCTLRALNTVADLLSPKSTL 299
Qy 765 RAMAAKTVCPHAKVELELLE-----KQAYKEQVLAKRLTMLELEKYPACMEKSFELL-AL 820
Db 300 LAAAHASDTEADRLQFLASREGKDEYEMIVANORSLLEWAEAPPAPPLGVFPAAI 359
Qy 821 LPSIRPRYSISSPRVDEKQASITVSVSGEAMSGVEGKIASNYL-----LAELOEG 874
Db 360 APRQEPRTYISSPPKVPENRINHVTALVY-ETPGGRIRHKICSTMKKAVALPTEHQDC 418
Qy 875 DITTCFISTPOSEFTLPKDEPRLINVGPGTVAPRFGVQARKOLKEQOSLGEAHLTF 934
Db 419 SSAPIFVRT--SNPRLPADPKVPMVIGPBTGLAPRFGIQLERAWLRQGEKVEGTLVLYGC 476
Qy 935 GCSPHEDLYOELENAOSEGIIT-LHTAFSMPNOPKTYVOHVMEOGDKLIELLDGAAH 993
Db 477 GCRNRKVDFTYENELNNFENGALSELDMAFSR-EGASKEVYVQHKNSQKASDIWMLSEG 535
Qy 994 AHFYICGDSQMAPAVEATLMSYADVHOVSEADARLMLQLEBKGRYAKDWA 1046
Db 536 AYLYVCGDARNMARDVONTFYDVLAEIGMEHAQAVDIKMLTKGRYSLDVAWS 588

```

## RESULT 3

```

US-10-224-249-14
: Sequence 14, Application US/10224249
: Publication No. US20030087867A1
: GENERAL INFORMATION:
: APPLICANT: Vogels, Ronald V.
: TITLE OF INVENTION: Gene therapy for enhancing and/or inducing angiogenesis
: FILE REFERENCE: 2183-5233US
: CURRENT APPLICATION NUMBER: US/10/224,249
: CURRENT FILING DATE: 2002-08-19
: PRIOR APPLICATION NUMBER: PCT/NL00/00482
: PRIOR FILING DATE: 2000-07-07
: PRIOR APPLICATION NUMBER: EP 99202263.2
: PRIOR FILING DATE: 1999-07-09
: PRIOR APPLICATION NUMBER: US 60/143,101
: PRIOR FILING DATE: 1999-07-09
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 14
: LENGTH: 1433
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CHAIN
: LOCATION: (1)..(1433)
: OTHER INFORMATION: Human nitric oxide synthase
US-10-224-249-14

```

Query Match 12.4%; Score 675; DB 9; Length 1433;  
 Best Local Similarity 28.0%; Pred. No. 1.2e-40;  
 Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

```

Qy 457 GIPSPSTEGSAAKVRKAAE-----NAHNPRLVLVYSNMGTACTARDLADIA 504
Db 722 GTNGTPFKRAAIFKKLAEVKFSAKLMGQAMKRVYATLLVATETGKSOAVAKTLCET 780
Qy 505 MSKGAPAVQVATLDSH-AGNLPREGAVLITVASY-NGHPPDNMAKOF----- 547
Db 781 FKXAFDAKWSMEYDVLVHLEHETLVVVTSTGNGDPPRNGKFGCALKMEMHNSVOE 840
Qy 548 -----VDWLDQ-ASADEVKSVRYSVFGCDKRMWATTYQV 581
Db 841 ERSKYKVRNVSYSYSDQSGDGPLRDNFESAGPLANVRFSVGLGSR-----AVPHF 896
Qy 582 PAF---IDETLLAKAENIADRGADASDDEFGTYEERHMSDVAAYVNL--DIENSE 636
Db 897 CAFGHAVDTLLEELGGERILMKREGDELCOGEAFAFTWAKKVAACDVFCVDDVNIK 956

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QY 637 DNKSTLS-----LQFVDSAADMP--LAKMH--GAFSTNVASKELQPGSARST 681  
 DB 957 ANNSLSINDSWKNRKRRLTFVAEAPRLTQGLSNVHKRVSAAARLSRQLQSKSRST 1016  
 QY 682 RHLEIEL--PKXASYQBGDLGVIPRNYEGIVNRVTARFGLDA--SQQIRLEAEEK-- 734  
 DB 1017 IFRHLTNGSQEOLQYOPGDHLGVFPGNHEDLVNALLERLE-DAPRVNQMVLEERNT 1075  
 QY 735 -----LHHLPLAKTVSVELLQVYELQDPVTRTOLRAMAKTVCPHKVLEALLE- 765  
 DB 1076 ALAVISNMTDELRLPCTTFOAFRYADITTPPLQLOQPASLASEKQRLVLVSKG 1135  
 QY 786 KQAYKEQVLAKRLTMLLEKRYPACEMKFSEFIALPSIRPRYSSISSPRVDEKQASIT 845  
 DB 1136 LQGYEEMKKNKPTIVEVLEEPSIQMPATLLTQSLQPRYSSISSSDMDVDEVHLT 1195  
 QY 846 VSVVSGEAMSGYB-YKGIASNYLAELQEGDTTTCISTPOSEFTLPKDPETPLIMVPG 904  
 DB 1196 VAVISYTRDGEGRPHHGVCSWLNRIQADELVPCFRGAPS-FHLPRNQVPCILVPG 1254  
 QY 905 TGVAPRGCFVQARK-QKKEGQSGEALYFGCSPHEDLVQOELENAQSEGIT-TLHT 962  
 DB 1255 TGIAPRFSFWQOFDIOHGKMPCPVILVFGCKQSKIDHLYREETLQAKNKGVFRELYT 1314  
 QY 963 AFGRMPNQPTVYQVHWEODGKLI--ELPDGAFHYICGDSQMAPAVEATLMKSYADV 1020  
 DB 1315 AYSGEDPKPKVYQDILQEBLAEVYRALKEGGHYVCGDYMAADVLA--IQRIMTQ 1373  
 QY 1021 HOVSEADARLMLQLEEKRYAKDV 1046  
 DB 1374 GKLSAEDAGVVISRMDNRHYEDIF 1399

## RESULT 4

US-09-870-759-124  
 ; Sequence 124, Application US/09870759  
 ; Patent No. US20020177551A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TERMAN, David S  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
 ; FILE REFERENCE: 870759  
 ; CURRENT APPLICATION NUMBER: US/09/870,759  
 ; CURRENT FILING DATE: 2002-01-14  
 ; PRIOR APPLICATION NUMBER: US 60/208,128  
 ; PRIOR FILING DATE: 2000-05-30  
 ; NUMBER OF SEQ ID NOS: 166  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 124  
 ; LENGTH: 1144  
 ; TYPE: PRF  
 ; ORGANISM: Mus musculus  
 ; US-09-870-759-124

Query Match 12.2%; Score 665.5; DB 9; Length 1144;  
 Best Local Similarity 31.6%; Pred. No. 4.2e-40;  
 Matches 191; Conservative 111; Mismatches 245; Indels 57; Gaps 25;

QY 484 VLYGSMWGTBEGARLADLADAMSKGAPQVATLDSH-AGNLPRGAVLITYASY-NGHPP 541  
 DB 535 VLPAETGKSEALARDLATL-FSYAFNTKVCMDQYKASTLEBOLLVVTSTFGNDCP 593  
 QY 542 DNA---KQFVDMIDQASADGVKGVSVFGCGDKMATTYQKPAF---IDETLAAGAE 595  
 DB 594 SNOGLTKKSLFMLELN---HTFRYAVFGLG---SSWYPOCAFADIDQKLSHGAS 645  
 QY 596 NIADRGADASDDEFGTEYEMREHMS-----DVAAYFNLDIENSNDKSTLSLQ---F 646  
 DB 646 QLAPTEGDELSGEDAFRSMVAQTFPACETFPVRSKHIIQPKRTSNATWEPQYRL 705  
 QY 647 VDSAAAD---PLAKMH--GAFSTNVASKELQPGSARST--HLEIELPKXASYQEGD 698  
 DB 706 IQSPEPLIDLRALSLIHAKVFTWRLKSOQLQSEKSRITLLVQLTFEGSRGSPSYLGE 765

QY 699 HLGVIPIRNYEGIVNRVTARFGLDA--SQQIRLEAEEK-----KLHPLAKTVSVEL 749  
 DB 766 HLGIFPGNGALVQGLIERV-VDCEPHQVTCLEVEDSSVWVKRRLP---PCSLSQ 821  
 QY 750 LQY-VELQDPVTRTOLRAMAKTVCPHKVLEALLEKQAYKEQVLAKRLTMLLEKYP 808  
 DB 822 LTYFLDITTPPTLOLHKLARFATDETRDRLBALQPSSEYNWKFSSNPTFVLEIEFP 881  
 QY 809 ACMEKSEFIALPSIRPRYSSISSPRVDEKQASITVSVSGEAMSGYB-YKGIASNY 867  
 DB 882 SLHVPAFLISQPLIKPRYSSISSQDHTPSSVHLVAVVYTRDQGPRLHGVSTW 941  
 QY 868 LAELQEGDTTTCISTPOSEFTLPKDPETPLIMVPGTGVAPRGVQAR-KQKKEGQS 926  
 DB 942 IRLKQODPVCPCVRS-VSGFQLPEDPSQPCILIGCTGIAPRFSFWQGRHDSQHGK 1000  
 QY 927 LGEAHLVFGCRSPHEDLVQOEL-ENAOSEGITTLHTAFGRMPNQPTVYQVHWE-QDGK 984  
 DB 1001 GGRMSLVFGCRSPHEDLVQOEWQEMVRKRVLFQVHTGYRLPGKPKVYVQDILQKOLAN 1060  
 QY 985 KLEIEL--DQGAHYICGDSQMAPAVEATLMKSYADVHOVSEADARLMLQLEEKRYA 1042  
 DB 1061 EVLSVLHGEQ-FLYTCGD-VRRADVATTLKLVATKMLSEQVEDYEFOLKSQRYH 1118  
 QY 1043 KDVM 1046  
 DB 1119 EDIF 1122

## RESULT 5

US-10-224-249-13  
 ; Sequence 13, Application US/10224249  
 ; Publication No. US20030087867A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vogels, Ronald V.  
 ; APPLICANT: Verilinden, Stefan F.F.  
 ; TITLE OF INVENTION: Gene therapy for enhancing and/or inducing angiogenesis  
 ; FILE REFERENCE: 2183-5233US  
 ; CURRENT APPLICATION NUMBER: US/10/224,249  
 ; CURRENT FILING DATE: 2002-08-19  
 ; PRIOR APPLICATION NUMBER: PCT/NL00/00482  
 ; PRIOR FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: EP 99202263.2  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: US 60/143,101  
 ; PRIOR FILING DATE: 1999-07-09  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 13  
 ; LENGTH: 1153  
 ; TYPE: PRF  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CHAIN  
 ; LOCATION: (1)-(1153)  
 ; OTHER INFORMATION: Homo sapiens inducible nitric oxide synthase  
 ; US-10-224-249-13

Query Match 11.9%; Score 650; DB 9; Length 1153;  
 Best Local Similarity 30.3%; Pred. No. 5.9e-39;  
 Matches 195; Conservative 112; Mismatches 272; Indels 64; Gaps 22;

QY 447 KASKKILPLGISTPSTEGSAKVRKA-----ENAHNTPLLVLYGSMWGTBEGT 496  
 DB 507 RPRRRRIPL-----KVLVKAVALFACMLMKRTWASVRVYTLIFATETGSEAL 553  
 QY 497 ARDLADIAMSKGAPQVATLDSH-AGNLPRGAVLITYASY-NGHPPDNKQFVMDQA 554  
 DB 554 AMDLGL-FSCAFNPVYCMCKYRLSCLEBERLLVVTSTFGNDCPGRGSKLSFLM 612  
 QY 555 SADEVKGVSYVFGCDKMWATTYQKPAF---IDETLAAGAENIADRGADASDDEFG 611

Db 613 KELNNK-FRYAVFGLG-----SMYPRFCAFAHDIDOKLSHGASQLTMPMEGDELSCQED 667

Qy 612 TYEEMREHMMS-----DVAAYFNLDIENSEDNKSTLS---LQFVDSADMPPLAK-----M 658

Db 668 AFRSMAYOTFKAACETEDVRGKHIOIPLKLYTSNVTMDPHHYRLVODSOPLDLSKALSSM 727

Qy 659 H-GAFSTNVVASKELOQPSASRSTRHLEI--ELPKASVYQEGDHLGVIPRNYEGIVNRV 714

Db 728 HAKVFTMRKSRQNLQSPSTSSRATILVELSCEDGGLNLPBHLGVCPGNQALVQGI 787

Qy 715 TARF--GLDASQOIRLEAEKEKLAHLPLAKTV---SVELLOQY-VELQDPVTRTQOLPAMA 768

Db 788 LERVDPDPTPHQTVRLLEDLDESGSYWSDKRLPPCSLSQALTYSPTDITPTPTOLLQKLA 847

Qy 769 AKTVCPRHKVELBALLEKQAYKEQVLAKRLTMELEKYPACEMKSEFIALPISIRPY 828

Db 848 QVATEEBERQRLBALCOPSEYSKMKFTNSPTFLEVEEPFLVSAGFLLSQILKPRF 907

Qy 829 YSISSSPRVDEKQASITVSVSGEAMSGYGE-YKGIASNYLAELQEGDITTCFISTPQSE 887

Db 908 YSISSSRDHPTPEIHLTVAVVTYHTGDGQGPLHHGVCSYTLNLSLKPDQPVPCFVRN-ASA 966

Qy 888 FTLPKQDETPILMVGPGTGVAPFRGFGVOAR-KOLKEQOSLGEAHLTFGCRSPHEDLYQ 946

Db 967 FHLPEDSHPCILIGPGTGIVPFRSFWOQRLHDSQHKVGVRGRTLVFGCRPDEDHIIQ 1026

Qy 947 EE-LENQSGEITLTHAFSRMNPQKTYVOHWMED--GKLIJELDOGAHFYICGDS 1003

Db 1027 EEMLEMAQKGLVAHVHTYRSLPGRPKYVODITLRQOLASVLRVHLKHEPRLHYCGD-V 1085

Qy 1004 QMAPAVEATLMKSYADVHQVSEADARLMLQOLEEKGAYKDVW 1046

Db 1086 RMRADVHTLKQOLVAALKKLNBEQVEDYFQLKSQKRYHEDIF 1128

RESULT 6

US-09-992-056-2

Sequence 2, Application US/09992056

Patent No. US20020061862A1

GENERAL INFORMATION:

APPLICANT: Billiar, Timothy R.

APPLICANT: Tzeng, Edith

APPLICANT: Nussler, Andreas K.

APPLICANT: Geller, David A.

APPLICANT: Simmons, Richard K.

APPLICANT: Shears II, Larry L.

TITLE OF INVENTION: Inducible Nitric Oxide Synthase Gene for Treatment of

TITLE OF INVENTION: Disease

FILE REFERENCE: 213298

CURRENT APPLICATION NUMBER: US/09/992,056

CURRENT FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: 09/176,496

PRIOR FILING DATE: 1998-10-21

PRIOR APPLICATION NUMBER: 08/465,522

PRIOR FILING DATE: 1995-06-05

PRIOR APPLICATION NUMBER: 08/314,917

PRIOR FILING DATE: 1994-09-28

PRIOR APPLICATION NUMBER: 07/981,344

PRIOR FILING DATE: 1992-11-25

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 1153

TYPE: PRT

ORGANISM: Induced Human Hepatocyte RNA

US-09-992-056-2

Query Match 11.9%; Score 650; DB 10; Length 1153;

Best Local Similarity 30.3%; Pred. No. 5.9e-39;

Matches 195; Conservative 112; Mismatches 272; Indels 64; Gaps 22;

Qy 447 KAKSKKIPLGIGIPBPTQSAKKYRKKA-----ENAHNTPLVLVYSSNMGTAECT 496

Db 507 RPKREIPL-----KVLKVAVLFACMLRKMTWASERVITLIFATETGSEAL 553

Qy 497 ARDLADIAMSGKGFAPVATLDSH-AGNLPREGAVILVTASY-NGHPDNKQCFVMDLQ 554

Db 554 AMLDGL-ESCANPKVYCMCKYRLSCLEEBRLLVVTSTFGNGDPCRGNEKUKLSIFML 612

Qy 555 SADEVKQVRSVFGCDKMMATTYQKVPF--IDETLAKGAENIADRGEADASDFEG 611

Db 613 KELNNK-FRYAVFGLG-----SMYPRFCAFAHDIDOKLSHGASQLTMPMEGDELSCQED 667

Qy 612 TYEEMREHMMS-----DVAAYFNLDIENSEDNKSTLS---LQFVDSADMPPLAK-----M 658

Db 668 AFRSMAYOTFKAACETEDVRGKHIOIPLKLYTSNVTMDPHHYRLVODSOPLDLSKALSSM 727

Qy 659 H-GAFSTNVVASKELOQPSASRSTRHLEI--ELPKASVYQEGDHLGVIPRNYEGIVNRV 714

Db 728 HAKVFTMRKSRQNLQSPSTSSRATILVELSCEDGGLNLPBHLGVCPGNQALVQGI 787

Qy 715 TARF--GLDASQOIRLEAEKEKLAHLPLAKTV---SVELLOQY-VELQDPVTRTQOLPAMA 768

Db 788 LERVDPDPTPHQTVRLLEDLDESGSYWSDKRLPPCSLSQALTYSPTDITPTPTOLLQKLA 847

Qy 769 AKTVCPRHKVELBALLEKQAYKEQVLAKRLTMELEKYPACEMKSEFIALPISIRPY 828

Db 848 QVATEEBERQRLBALCOPSEYSKMKFTNSPTFLEVEEPFLVSAGFLLSQILKPRF 907

Qy 829 YSISSSPRVDEKQASITVSVSGEAMSGYGE-YKGIASNYLAELQEGDITTCFISTPQSE 887

Db 908 YSISSSRDHPTPEIHLTVAVVTYHTGDGQGPLHHGVCSYTLNLSLKPDQPVPCFVRN-ASA 966

Qy 888 FTLPKQDETPILMVGPGTGVAPFRGFGVOAR-KOLKEQOSLGEAHLTFGCRSPHEDLYQ 946

Db 967 FHLPEDSHPCILIGPGTGIVPFRSFWOQRLHDSQHKVGVRGRTLVFGCRPDEDHIIQ 1026

Qy 947 EE-LENQSGEITLTHAFSRMNPQKTYVOHWMED--GKLIJELDOGAHFYICGDS 1003

Db 1027 EEMLEMAQKGLVAHVHTYRSLPGRPKYVODITLRQOLASVLRVHLKHEPRLHYCGD-V 1085

Qy 1004 QMAPAVEATLMKSYADVHQVSEADARLMLQOLEEKGAYKDVW 1046

Db 1086 RMRADVHTLKQOLVAALKKLNBEQVEDYFQLKSQKRYHEDIF 1128

RESULT 7

US-10-224-249-15

Sequence 15, Application US/10224249

Publication No. US20030087867A1

GENERAL INFORMATION:

APPLICANT: Vogels, Ronald V.

APPLICANT: Verlinden, Stefan F.F.

TITLE OF INVENTION: Gene therapy for enhancing and/or inducing angiogenesis

FILE REFERENCE: 2183-5233US

CURRENT APPLICATION NUMBER: US/10/224,249

CURRENT FILING DATE: 2002-08-19

PRIOR APPLICATION NUMBER: PCT/NL00/00482

PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: EP 99202263.2

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: US 60/143,101

PRIOR FILING DATE: 1999-07-09

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.1

SEQ ID NO 15

LENGTH: 1203

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CHAIN

LOCATION: (1)..(1203)

OTHER INFORMATION: Human nitric oxide synthase

US-10-224-249-15

Query Match 11.2%; Score 608.5; DB 9; Length 1203;

Best Local Similarity 26.7%; Pred. No. 7e-36;  
Matches 191; Conservative 115; Mismatches 254; Indels 155; Gaps 24;

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QY 454 PLGGIPSPTEGSAKKYRKAEN-----AHNPLVLIVGSMNGTEGARDL 500
DB 479 PMKGSAAKGGTIRKTKFKENAVANAKISALMGTMAKRKVATLTVGSETGRQSYAQQ 538
QY 501 ADIAMSKEAPQVATLDSH-AGNLPRGAVLITVASY-NGHPPDNAAQFV-----548
DB 539 GRV-FKAPDPRVLCMDYVVSLEHETLVLTSTFGNDPDPENGSSFLAALMMSGPY 597
QY 549 -----DW-----LDQASADEVKGVRYSVFCCGDKM 574
DB 598 NSSPREOHKSYKIRFNSISCSDDLVSWMRKREKESNTDSAGALGTLRFCEVGLGSR-- 655
QY 575 ATTYQVAPF---IDETLAAGAENIADRGADASDFEGTYEEMHMSDVAAAFNLD 631
DB 656 --AHPFCAPARAVDTRLEELGGBRLQLQGBELCGQEBAPFGMAQAAQAAACEFV- 712
QY 632 IENSEDNKSTL-----SLQFVDSAADMPLAKMHGAFSTNVAS 669
DB 713 ---GEAKAARADIFSPKRSWKQRYRLSQAAGLQLPGLIHVHRKM---FOATIRSV 766
QY 670 KELQPGASRSTRHLEIEL--PKASYQESDHLGVIPRNYEGIVNRYTARFGLDASQQR 727
DB 767 ENIQSSKSTRATILVLDTCGQEGQLQYQPGDHLGVCPNRPGLVEALSR-----816
QY 728 LEAEERKLAHLPLAKT--VSVEELQ-----YVELQDP 758
DB 817 -VED-----PAPFEPAVEQLEKSGPGGPPGVWRDRLPPTLRQALTFELDTSP 868
QY 759 VTRTOLRAMAKTVCPPHKVELEAL-LEKQAYKEQVLAKRLTMLLEKRYPACEMKFSER 817
DB 869 PSQQLRLSTLAEPREQOELEALSODPRRYEEMKFRCPITLLEVLEQPSVALPAPL 928
QY 818 IALLPSIRPRYYSISSPRVDEKQASITVSVSGEAMSGYGE-YKGIASNYLAELQEDT 876
DB 929 LTQLPLQPRYVSVAAPSTHPEIHLTVAVLAVRTQDGLGPLHYGVCSTWLSQLKXDP 988
QY 877 ITCEFTPQSEFTLPDPEFTPLIMGCGTGVAPRGVQAR-KQKEQGSLSBAHLFYG 935
DB 989 VPCFINGAPB-FLLPDPSPCLVPGGTIAPRGWQORLHDIKSGLOPTPMTLVFG 1047
QY 936 CRSPHEDYLYQOELENAQSEGI-THATASRMPNOQPTVVOHMEQDGKLE---LLD 991
DB 1048 CRCSQDLHLYRDEVQAQCGVGRVLTASRBDNKXTVVDILKRELAAEVRVLCLE 1107
QY 992 QGAHFYICGDSQMAPAVEATLMKSYADVHQVSEADARLMLQOLEEKGRYAKDVW 1046
DB 1108 RG-HMEVCCDVT-MATVVLQTVORILATEGMELDEAGDIVIGVLRDQORYHEDIF 1160

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## RESULT 8

```

US-10-138-838-117
; Sequence 117, Application US/10138838
; Publication No. US20030049821A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Escho, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Teng, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138, 838

```

CURRENT FILING DATE: 2002-05-03  
PRIOR APPLICATION NUMBER: US/09/976, 800  
PRIOR FILING DATE: 2001-10-12  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 117  
LENGTH: 679  
TYPE: PRT  
ORGANISM: CANDIDATROPICALIS  
US-10-138-838-117

Query Match 11.0%; Score 598; DB 9; Length 679;  
Best Local Similarity 27.2%; Pred. No. 1.8e-35;  
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

```

QY 430 ELIDIKETLLKBPFGVVRKSKKI-----PLGGIPSPTEGSAKKYRKAENAHNTLLVL 485
DB 5 KLDLVYITLVVAVAAYFAKNQFLDQPDQDTGFLNTDSGNSRDVSTLTKNNKNT--LLL 62
QY 486 YGSNMGTAGTARDLADIAMSK-GFAPQVATLDSH-----AGNLPRGAVLITVASY-NGH 539
DB 63 FSGQGTADYANKLSRELHSRGLKTVNADPADYDMNFGDITEDILVFFIATYGBGE 122
QY 540 PPDNAQFVDWLDQASADEVKGVRYSVFCCGDKMATTYQKVPF---IDETLAAGAEN 596
DB 123 PTDNADEFHTWLTE-BADTLSTLKTVFGIGN---STVEFNAIGRKFDRLLEKGDGR 177
QY 597 IADRGADASDDEPGYEE---WRHMSDVAAAFNLD-----631
DB 178 FAEYAE---GDBGTGLEDLDFAMAKNDVFDALNDLNFEBEKELKYPNVKLTERRDLSAA 234
QY 632 ---IENSEDNKSTLSLQFVDSAADMPLAKMHGAFSTNVASKELOQPGASRSTRHLEIEL 688
DB 235 DGVSLGEBNKKYINSEGIDLTGK-PFDHTH-PYLARIETRELFS-SKDRHCHIVEFDI 291
QY 689 PK-EASYQEGDHLGVIPRNYEGIVNRYTARFGLDASQQRILEAE-EKLAHLPLAKTVASV 746
DB 292 SESNLKTYTGDHLAIWPSNSDENIKQFACFGLEDLDTVIELKALDSYTYIIPFPITY 351
QY 747 BELLO-Q-YVELQDPVTRTOLRAMAKTVCPPHKVELEAL---EKQAYKEQVLAKRLTML 801
DB 352 GAVIRHHLISGVSQFPLSLAG---FAPDETKKAFRLGDKQEFKAKYTRKXFNIA 408
QY 802 ELL-----EKYPACEMKFSFIALPISIRPRYYSISSPRVDEKQASITVSVSGEAMSGY 857
DB 409 DALIYSNNAPMSDVFEFLIENVPHLTRIYYSISS-SLSEQLINVTAVVAEAEADG 467
QY 858 GEYKGIASNYLAELQ-----EGDTITCFISTP-----OSEFTLPKDPET 896
DB 468 RPYTVGVVTLNKLKVEIVQKTEKPLVHYDLSGPRKFKFLPVHRRSNFGLPKNSTT 527
QY 897 PLIMVGRTGVAPFRGFVQARQKQKEQOSLSBAHLFYGCRSPHEHYLYQEE-LENAOSE 955
DB 528 PVLILGPGTVAPFLKRFVREVRVQVNGVNGVGTLLTFYCCRSNDEFLYKQEAEEASVYL 587
QY 956 G-IITHTAFSRMPNOQPTVVOHMEQDGKJLELDQGAHFYICGDSQMAPAVEATLM 1014
DB 588 GENFEMFNAPFSKODPEBKTYVQDKILENSQVHLELLEGAIIYVCGDASRMARDVQTTIS 647
QY 1015 KSYADVHQVSEADARLMLQOLEEKGRYAKDVW 1046
DB 648 KIVAKGREISEDKAELVSMKQVQNYQEDVW 679

```

## RESULT 9

```

US-10-139-031-117
; Sequence 117, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Escho, Mark

```

APPLICANT: Madduri, Krishna M.  
 APPLICANT: Cornett, Cathy A.  
 APPLICANT: Brenner, Alfred A.  
 APPLICANT: Tang, Maria A.  
 APPLICANT: Loper, John C.  
 APPLICANT: Gleeson, Martin  
 TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
 TITLE OF INVENTION: P450 OXIDOREDUCTASE  
 TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C  
 TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
 FILE REFERENCE: 1010-16  
 CURRENT APPLICATION NUMBER: US/10/139,031  
 CURRENT FILING DATE: 2002-05-03  
 PRIOR APPLICATION NUMBER: US/09/976,800  
 PRIOR FILING DATE: 2001-10-12  
 NUMBER OF SEQ ID NOS: 118  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 117  
 LENGTH: 679  
 TYPE: PRT  
 ORGANISM: CANDIDATROPICALIS  
 US-10-139-031-117

Query Match 11.0%; Score 598; DB 9; Length 679;  
 Best Local Similarity 27.2%; Pred. No. 1.8e-35;  
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

430 ELDIKELTLKPGFVAVAKSKI-----PLGGIPSPTEOSAKVKRKAENANTPLVL 485  
 5 KLDYVITITLVAAVAFAKQFLDQPDQDTGFLNTDSGNSRDVLTSLKKNKNT--LL 62  
 486 YGSNMGTAEGTARDLADIAISK-GFAPQVATLDSH---AGNLPREGAVLIVTASY-NGH 539  
 63 FGSQGTAEADYANKLSRELHSRFGKTMVADPADYDMNFGDITIEDILVFIVATYGE 122  
 540 PPDKAQFVWMLDQASADEVKGVRYISVFGCGDKMATTYQKVPF--IDETLAKEAN 596  
 123 PTDNADDFHTWLTE-EADTLSTLKYTVFGLGN---STVEFFNAIGRKFRLLSEKGGDR 177  
 597 IADGEADADDFEGTVEE---WREHMSDVAAVFLD----- 631  
 178 FAETAE--GDDGTGTLDEDFMAKQVFDALKNDLNEEKEKLYEPNVKLTERRDISAA 234  
 632 ---IENSDNKSTLSLOFVDSADMPPLAKMGAFTNVVASKELQOPGASRSTRHLEIEL 688  
 235 DSQVSLGEPNKKYINSEGDILTKG-PEDHTH-PYLARTETRELFS-SKORHCHIVERDI 291  
 689 PK-EASTQEGDHLCVIRNVEGIVNRVTARFGDASQOIRLEABE-EKLAHLPLAKTVSV 746  
 292 SESNLYKTTGDHLAIWPSNSDENIKQFAKCFGLDKLDTVIELKALDSTYTIPEPTPTY 351  
 747 EELLQ-VELODPYTRQLRAMAKTVCPRPKVLEALL-----EKOAYKEQVLAERLML 801  
 352 GAVIRHHLISGVPVSRQPFSLIAG--FAPDEETKATRLTGLGDKQEPAAVTRKRKNIA 408  
 802 ELL-----EKYPACEMKSEFIALPLSIRPRYYSISSSPRVDEKQASITVSVSGEANSY 857  
 409 DALYSSNNAWMSDVPEFLIENPHLTRYYSISS--SLSEKQIINTAVAVEABEADG 467  
 858 GEYGIASNYLAELO-----EGDTTCFISTP-----QSEFTLPKQDET 896  
 468 RPYGVGVNMLKNEVEIYONKTGEKPLVHYDLSGPRGKFNKFLPVHVRSSFKLPKQSTT 527  
 897 PLIIVGPGTGVAPRPGVQARKOLKEQOSLGEAHLVYGCSPHEDVLYORE-LENAQSE 955  
 528 PVLILGPGTGVAPRPGVQARKOLKEQOSLGEAHLVYGCSPHEDVLYORE-LENAQSE 955  
 956 G-IITLTAFSRMPNQPTVYVQHVMEODGKLIIEILDGAFYICGDSQNAVAVETIM 1014  
 588 GENEMFNAFGRQDSKVVYVQDKLENSQLVHLELTGALIIYVCGDASRNARDVQTTIS 647  
 1015 KSYADVHOVSADARLMLQOLEEKGRVAKDYW 1046

Db 648 KIVAKSREISEDKAAELVSKWQVONRYOEDVW 679

# RESULT 10

US-10-138-905-117  
 Sequence 117, Application US/10138905  
 Publication No. US20030068800A1  
 GENERAL INFORMATION:

APPLICANT: Craft, David L.  
 APPLICANT: Wilson, Ron C.  
 APPLICANT: Birch, Dudley  
 APPLICANT: Eshoo, Mark  
 APPLICANT: Madduri, Krishna M.  
 APPLICANT: Cornett, Cathy A.  
 APPLICANT: Brenner, Alfred A.  
 APPLICANT: Tang, Maria  
 APPLICANT: Loper, John C.  
 APPLICANT: Gleeson, Martin  
 TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
 TITLE OF INVENTION: P450 OXIDOREDUCTASE  
 TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C  
 TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
 FILE REFERENCE: 1010-16  
 CURRENT APPLICATION NUMBER: US/10/138,905  
 CURRENT FILING DATE: 2002-05-03  
 PRIOR APPLICATION NUMBER: US/09/976,800  
 PRIOR FILING DATE: 2001-10-12  
 NUMBER OF SEQ ID NOS: 118  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 117  
 LENGTH: 679  
 TYPE: PRT  
 ORGANISM: CANDIDATROPICALIS  
 US-10-138-905-117

Query Match 11.0%; Score 598; DB 9; Length 679;  
 Best Local Similarity 27.2%; Pred. No. 1.8e-35;  
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

430 ELDIKELTLKPGFVAVAKSKI-----PLGGIPSPTEOSAKVKRKAENANTPLVL 485  
 5 KLDYVITITLVAAVAFAKQFLDQPDQDTGFLNTDSGNSRDVLTSLKKNKNT--LL 62  
 486 YGSNMGTAEGTARDLADIAISK-GFAPQVATLDSH---AGNLPREGAVLIVTASY-NGH 539  
 63 FGSQGTAEADYANKLSRELHSRFGKTMVADPADYDMNFGDITIEDILVFIVATYGE 122  
 540 PPDKAQFVWMLDQASADEVKGVRYISVFGCGDKMATTYQKVPF--IDETLAKEAN 596  
 123 PTDNADDFHTWLTE-EADTLSTLKYTVFGLGN---STVEFFNAIGRKFRLLSEKGGDR 177  
 597 IADGEADADDFEGTVEE---WREHMSDVAAVFLD----- 631  
 178 FAETAE--GDDGTGTLDEDFMAKQVFDALKNDLNEEKEKLYEPNVKLTERRDISAA 234  
 632 ---IENSDNKSTLSLOFVDSADMPPLAKMGAFTNVVASKELQOPGASRSTRHLEIEL 688  
 235 DSQVSLGEPNKKYINSEGDILTKG-PEDHTH-PYLARTETRELFS-SKORHCHIVERDI 291  
 689 PK-EASTQEGDHLCVIRNVEGIVNRVTARFGDASQOIRLEABE-EKLAHLPLAKTVSV 746  
 292 SESNLYKTTGDHLAIWPSNSDENIKQFAKCFGLDKLDTVIELKALDSTYTIPEPTPTY 351  
 747 EELLQ-VELODPYTRQLRAMAKTVCPRPKVLEALL-----EKOAYKEQVLAERLML 801  
 352 GAVIRHHLISGVPVSRQPFSLIAG--FAPDEETKATRLTGLGDKQEPAAVTRKRKNIA 408  
 802 ELL-----EKYPACEMKSEFIALPLSIRPRYYSISSSPRVDEKQASITVSVSGEANSY 857  
 409 DALYSSNNAWMSDVPEFLIENPHLTRYYSISS--SLSEKQIINTAVAVEABEADG 467  
 858 GEYGIASNYLAELO-----EGDTTCFISTP-----QSEFTLPKQDET 896

Db 468 RPYTGVVTLNKKVEIVQNTGKPLVHYDLSGPRGKFNKFLPVHVRSGNFKLPKXSTT 527  
 Qy 897 PLIMVPGTGVAPFRGTVQARKOLKEQOSLGEAHLYFGCRSPHEDLYOEB-LENAOSE 955  
 Db 528 PVLIGGTGTVAPLRGVRERVOQVGVNGVNGKTLTYGCRNSHEDFLYQENAEYASVL 587  
 Qy 956 G-IITHTAFSRMNPQKTYVQVHMEODGKKLIELLDQGAHFIYICGDSQMAPAVEATLM 1014  
 Db 588 GENFEMFNARSRODPSKVVYVQDKLIENSQVHLLTEGAIIYVCGDASMRADVQTTIS 647  
 Qy 1015 KSYADVHVSSEADARLMLQOLEEKGRYADVM 1046  
 Db 648 KIVAKSREISEDKAELVSKMVKQNRQYQEDVM 679

RESULT 11  
 US-10-138-916-117  
 ; Sequence 117, Application US/10138916  
 ; Publication No. US20030073220A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wilson, Ron C.  
 ; APPLICANT: Craft, David L.  
 ; APPLICANT: Eirich, Dudley  
 ; APPLICANT: Eshoo, Mark  
 ; APPLICANT: Madhuri, Krishna M.  
 ; APPLICANT: Cornett, Cathy A.  
 ; APPLICANT: Brenner, Alfred A.  
 ; APPLICANT: Tang, Maria  
 ; APPLICANT: Loper, John C.  
 ; APPLICANT: Gleeson, Martin  
 ; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE  
 ; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C. TROPICALIS  
 ; FILE REFERENCE: 1010-16  
 ; CURRENT APPLICATION NUMBER: US/10/138,916  
 ; CURRENT FILING DATE: 2002-05-03  
 ; PRIOR APPLICATION NUMBER: 09/976,800  
 ; PRIOR FILING DATE: 2001-10-12  
 ; PRIOR APPLICATION NUMBER: US 09/302,602  
 ; PRIOR FILING DATE: 1999-04-30  
 ; NUMBER OF SEQ ID NOS: 118  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 117  
 ; LENGTH: 679  
 ; TYPE: PRT  
 ; ORGANISM: CANDIDATROPICALIS  
 ; US-10-138-916-117

Query Match 11.0%; Score 598; DB 9; Length 679;  
 Best Local Similarity 27.2%; Pred. No. 1.8e-35;  
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

Qy 430 ELDIKELTLTKPEGFVVKAKSKI-----PLGGIPSPSTEGSAKKVRKKAENANTPLVLV 485  
 Db 5 KDLVLYIITLVVAVAFAKQFLDPODQDTGFLNTSGNSRDLSTLKKXNKT--LL 62  
 Qy 486 YGSNMGTAEGTADLADIAMS-K-GFAPQVATLDSH-----AGNLPREGAVLIVTASY-NGH 539  
 Db 63 FGSOTGTAEDYANKLSRELHRSRGLKTMVADPADYDMNFGDITEDILVFIVATYGEGB 122  
 Qy 540 PPDNAQFVMDLQASADEVKGRYSVFGCGDKMAATTYQKPAF--IDETLAAGAEN 596  
 Db 123 PTDNADFTWLT-E-ADDTLSTLKYTVFGN-----STYEFNNAIGKFRLLSEKGGDR 177  
 Qy 597 IARGEDADSDDEFGTYE-----WREHMSDVAAVFLD----- 631  
 Db 178 FAAYAE---GDDGTGLTDEDFMAKQNVFDALKNKDLNFEKEKLYEBNVLTERRDLSSA 234  
 Qy 632 ---IENSDEKSTLSLOFVDSADMPKAKMGAFSTNVVASKELQCGASRSTRHLEIL 688  
 Db 235 DSQVSLGEPRKXKYSNGSILTKG-PEDRTH-PLAIIITTRHIFS-SKRHCCHVEFDI 291  
 Qy 689 PK-EASYQEGDHLGVI-PRNVEGIIVNRVTARFGLDASQIRLEABE-EKLAHLPLAKTVSV 746

Db 292 SESNLKYYTGDLHAIWPSNSENENIKQFACFCGLEDLDFVIELKALDSTYITPPTITY 351  
 Qy 747 EELLQ-VYELQDPVTRQLRAMAKVCPPHKLEALL-----EKQAYNEQVLAKLTM 801  
 Db 352 GAVIRHLEISGVSRQFLISAG---FADETKKAFTRLGGDKQFAKVRKRNFA 408  
 Qy 802 ELL-----EKYPACEMFSEPIALLPSIRPRYSISSPRVDEQASITVSGEAMSGY 857  
 Db 409 DALYSSNAPWSDVFEFLIENVPHLTRYSISS-SISEQOLNVAVVAEEDAG 467  
 Qy 858 GEYKIASNYLAELQ-----EGDTITCFISTP-----OSEFTLPKDPET 896  
 Db 468 RPYTGVVTLNKKVEIVQNTGKPLVHYDLSGPRGKFNKFLPVHVRSGNFKLPKXSTT 527  
 Qy 897 PLIMVPGTGVAPFRGTVQARKOLKEQOSLGEAHLYFGCRSPHEDLYOEB-LENAOSE 955  
 Db 528 PVLIGGTGTVAPLRGVRERVOQVGVNGVNGKTLTYGCRNSHEDFLYQENAEYASVL 587  
 Qy 956 G-IITHTAFSRMNPQKTYVQVHMEODGKKLIELLDQGAHFIYICGDSQMAPAVEATLM 1014  
 Db 588 GENFEMFNARSRODPSKVVYVQDKLIENSQVHLLTEGAIIYVCGDASMRADVQTTIS 647  
 Qy 1015 KSYADVHVSSEADARLMLQOLEEKGRYADVM 1046  
 Db 648 KIVAKSREISEDKAELVSKMVKQNRQYQEDVM 679

RESULT 12  
 US-09-976-800-117  
 ; Sequence 117, Application US/09976800  
 ; Publication No. US2003007795A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wilson, Ron C.  
 ; APPLICANT: Craft, David L.  
 ; APPLICANT: Eirich, Dudley  
 ; APPLICANT: Eshoo, Mark  
 ; APPLICANT: Madhuri, Krishna M.  
 ; APPLICANT: Cornett, Cathy A.  
 ; APPLICANT: Brenner, Alfred A.  
 ; APPLICANT: Tang, Maria  
 ; APPLICANT: Loper, John C.  
 ; APPLICANT: Gleeson, Martin  
 ; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE  
 ; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C. TROPICALIS  
 ; FILE REFERENCE: 1010-16  
 ; CURRENT APPLICATION NUMBER: US/09/976,800  
 ; CURRENT FILING DATE: 2001-10-12  
 ; NUMBER OF SEQ ID NOS: 118  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 117  
 ; LENGTH: 679  
 ; TYPE: PRT  
 ; ORGANISM: CANDIDATROPICALIS  
 ; US-09-976-800-117

Query Match 11.0%; Score 598; DB 9; Length 679;  
 Best Local Similarity 27.2%; Pred. No. 1.8e-35;  
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

Qy 430 ELDIKELTLTKPEGFVVKAKSKI-----PLGGIPSPSTEGSAKKVRKKAENANTPLVLV 485  
 Db 5 KDLVLYIITLVVAVAFAKQFLDPODQDTGFLNTSGNSRDLSTLKKXNKT--LL 62  
 Qy 486 YGSNMGTAEGTADLADIAMS-K-GFAPQVATLDSH-----AGNLPREGAVLIVTASY-NGH 539  
 Db 63 FGSOTGTAEDYANKLSRELHRSRGLKTMVADPADYDMNFGDITEDILVFIVATYGEGB 122  
 Qy 540 PPDNAQFVMDLQASADEVKGRYSVFGCGDKMAATTYQKPAF--IDETLAAGAEN 596  
 Db 123 PTDNADFTWLT-E-ADDTLSTLKYTVFGN-----STYEFNNAIGKFRLLSEKGGDR 177

QY 597 IADRGADASDDPEGYEE---WREHMSDVAAYFNLD----- 631  
 Db 178 FAFAE---GDDGTGLDEDFPMKNDVFDALKNDLNFEEKELKYEPNVKLTERDLSAA 234  
 QY 632 ---IENSDNKSTLSLOFVDSADMPPLAKMGAFSTNVASKELQOPGASRSTRHLEL 688  
 Db 235 DSQVSLGEPNKKYINSEGDILTKG-PEDHTH-PYLARITETRELFS-SKDRHCIHVEFDI 291  
 QY 669 PK-EASYOEGDHLVIRPNVEGIVNRVTARFGLDASQOIRLEAE-EKLAHLPLAKTVSV 746  
 Db 292 SESNLKTTTGDHLAIWPSNDSNENIKOPAKCFGLDKLDVIELKALDSTYTFPPPTTY 351  
 QY 747 EELQ-YVELQDPTRTQLRAMAATVCPHKELEALL---EKQAYKEQVLAKEKLTML 801  
 Db 352 GAVIRHHLIEISGPRSQFLSING---FAPDETKKAFTRLGSGKQEPAAVTRKRNIA 408  
 QY 802 ELL---EKYPACEMKSEFIALPSTRPRYSSISSPRVDEKQASTVSVSGEAMSGY 857  
 Db 409 DALYSSNNAPMSDVPFEFLIENVPHLTPRYSSISS-SLSEKQILNVTAVVAEEADG 467  
 QY 858 GEYKGIASNYLAELQ-----EGDTITCFISTP-----OSEFTLPKDPE 896  
 Db 468 RPTVGTAVTNLKNVEIYONKTGEKPLVHYDLSGPRKFNKFLPVHVRNSFPLPKNSTT 527  
 QY 897 PLIMVGPSTGVAAPRFGFVOARKQKQOSLGEMHLYFGCRSPHEDLYOEE-LENAOSE 955  
 Db 528 PVLIGGTGVALPRGFRERVOQVKNGVNKTLLFYGCNSNEDFLYKQEMAEVASYL 587  
 QY 956 G-IITLHTAFSRMPNQPKTYQVHMEDDGKLELIDOGAHFYICGDSGMAVAEATLM 1014  
 Db 588 GENFEMFAFSRDPSPSKVYVODKILENSQLVHELLEGALIIYCGDASRMARDVQTTIS 647  
 QY 1015 KSYADVHQSSEADARLMLQOLEEKGAYKDVW 1046  
 Db 648 KIYAKSREISEDQAELVYSKWVQNRVQEDVW 679

RESULT 13  
 US-10-138-838-83  
 ; Sequence 83, Application US/10138838  
 ; Publication No. US20030049822A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wilson, Ron C.  
 ; APPLICANT: Craft, David L.  
 ; APPLICANT: Birch, Dudley  
 ; APPLICANT: Esboo, Mark  
 ; APPLICANT: Madduri, Krishna M.  
 ; APPLICANT: Cornett, Cathy A.  
 ; APPLICANT: Brenner, Alfred A.  
 ; APPLICANT: Tang, Maria  
 ; APPLICANT: Loper, John C.  
 ; APPLICANT: Gleeson, Martin  
 ; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
 ; TITLE OF INVENTION: P450 OXIDOREDUCTASE  
 ; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C  
 ; FILE REFERENCE: 1010-16  
 ; CURRENT APPLICATION NUMBER: US/10/138,838  
 ; CURRENT FILING DATE: 2002-05-03  
 ; PRIOR APPLICATION NUMBER: US/09/976,800  
 ; NUMBER OF SEQ ID NOS: 118  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 83  
 ; LENGTH: 679  
 ; TYPE: PRT  
 ; ORGANISM: CANDIDATROPICALIS  
 US-10-138-838-83

Query Match 10.9%; Score 597; DB 9; Length 679;  
 Best Local Similarity 27.2%; Pred. No. 2,1e-35;  
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

QY 430 ELDIKETLLTPREGFVYVAKSKKI-----PLGGIISPSTEQSAAKVRKKAENANHTLVLV 485  
 Db 5 KDLVYIITLIVAAVFAKNGFLDQRPDTGFLNTDSGSSRVLTLTKNNKNT--LL 62  
 QY 486 YGSNMGTAEGBADLADIAMSK-GFAPQVATLDH---AGNLPRGAVLITVAST-NGH 539  
 Db 63 FGSQGTGAEDYANKLREHLRSRGLKTMVADFADYMDNFDGDTIEDILVFFIATVGEGE 122  
 QY 540 PPNNAQFVWMLQOASADEYKGVSVFGGDNMAVTTQKQPAF---IDETLAAGAEN 596  
 Db 123 PTNADPFHTLWE-EDDTITLTKTYFGLGN---STIEFFNALGRKDRLLSEKGGDR 177  
 QY 597 IADRGADASDDPEGYEE---WREHMSDVAAYFNLD----- 631  
 Db 178 FAFAE---GDDGTGLDEDFPMKNDVFDALKNDLNFEEKELKYEPNVKLTERDLSAA 234  
 QY 632 ---IENSDNKSTLSLOFVDSADMPPLAKMGAFSTNVASKELQOPGASRSTRHLEL 688  
 Db 235 DSQVSLGEPNKKYINSEGDILTKG-PEDHTH-PYLARITETRELFS-SKDRHCIHVEFDI 291  
 QY 669 PK-EASYOEGDHLVIRPNVEGIVNRVTARFGLDASQOIRLEAE-EKLAHLPLAKTVSV 746  
 Db 292 SESNLKTTTGDHLAIWPSNDSNENIKOPAKCFGLDKLDVIELKALDSTYTFPPPTTY 351  
 QY 747 EELQ-YVELQDPTRTQLRAMAATVCPHKELEALL---EKQAYKEQVLAKEKLTML 801  
 Db 352 GAVIRHHLIEISGVSQFLSING---FAPDETKKAFTRLGSGKQEPAAVTRKRNIA 408  
 QY 802 ELL---EKYPACEMKSEFIALPSTRPRYSSISSPRVDEKQASTVSVSGEAMSGY 857  
 Db 409 DALYSSNNAPMSDVPFEFLIENVPHLTPRYSSISS-SLSEKQILNVTAVVAEEADG 467  
 QY 858 GEYKGIASNYLAELQ-----EGDTITCFISTP-----OSEFTLPKDPE 896  
 Db 468 RPTVGTAVTNLKNVEIYONKTGEKPLVHYDLSGPRKFNKFLPVHVRNSFPLPKNSTT 527  
 QY 897 PLIMVGPSTGVAAPRFGFVOARKQKQOSLGEMHLYFGCRSPHEDLYOEE-LENAOSE 955  
 Db 528 PVLIGGTGVALPRGFRERVOQVKNGVNKTLLFYGCNSNEDFLYKQEMAEVASYL 587  
 QY 956 G-IITLHTAFSRMPNQPKTYQVHMEDDGKLELIDOGAHFYICGDSGMAVAEATLM 1014  
 Db 588 GENFEMFAFSRDPSPSKVYVODKILENSQLVHELLEGALIIYCGDASRMARDVQTTIS 647  
 QY 1015 KSYADVHQSSEADARLMLQOLEEKGAYKDVW 1046  
 Db 648 KIYAKSREISEDQAELVYSKWVQNRVQEDVW 679

RESULT 14  
 US-10-139-031-83  
 ; Sequence 83, Application US/10139031  
 ; Publication No. US20030049822A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wilson, Ron C.  
 ; APPLICANT: Craft, David L.  
 ; APPLICANT: Birch, Dudley  
 ; APPLICANT: Esboo, Mark  
 ; APPLICANT: Madduri, Krishna M.  
 ; APPLICANT: Cornett, Cathy A.  
 ; APPLICANT: Brenner, Alfred A.  
 ; APPLICANT: Tang, Maria  
 ; APPLICANT: Loper, John C.  
 ; APPLICANT: Gleeson, Martin  
 ; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
 ; TITLE OF INVENTION: P450 OXIDOREDUCTASE  
 ; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C  
 ; FILE REFERENCE: 1010-16  
 ; CURRENT APPLICATION NUMBER: US/10/139,031  
 ; CURRENT FILING DATE: 2002-05-03  
 ; PRIOR APPLICATION NUMBER: US/09/976,800  
 ; PRIOR FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 118  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 83  
 LENGTH: 679  
 TYPE: PRT  
 ORGANISM: CANDIDATROPICALIS  
 US-10-138-031-83

Query Match 10.9%; Score 597; DB 9; Length 679;  
 Best Local Similarity 27.2%; Pred. No. 2,1e-35;  
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

QY 430 ELDIKETTLKPGFVVKAKSKKI---PLGGIPSPSTEOSAKVKRKAENAHNTPLVL 485  
 DB 5 KDLVYIITLVVAAYFAKNOFLDQPODPTGFLNTDGSNSRDVLLTLKKNKNT--LLL 62  
 QY 486 YGSNMGTAEGTADLADIAMSK-GFAPQVATLDH---AGNLPREGAVLITVASY-NGH 539  
 DB 63 FSGQTAEADYANKLSRELHSRGLTMTVADPADYMDNFGDITEDILVFIATYGEGE 122  
 QY 540 PPNNAQOFVMDLQDASADEVKGVRYSVFGGDKMATTYOKVPAF---IDETLAAGAEN 596  
 DB 123 PTNMADEFTWLTE-EADTLSTLKTIVFGLGN---STIEFFNAIGRKPRLLSEKGD 177  
 QY 597 IADRGADASDDEGTVEE---WREHMSDVAAYFNLD----- 631  
 DB 178 FAEYAE---GDDGTGLTDEDFPMAMKDNVPALKNDLNFEKEKLYEPNVKLTERRDL 234  
 QY 632 ---IENSDNKSTLSIQFVDSAADMPLAKHGAFTNVVASKELQPGSARSTRHLEIEL 688  
 DB 235 DSGVSLGEPNKKYINSBGIDLTGK-PFDHHT-PLYARITETRELFS-SKDRHCIHVEFDI 291  
 QY 689 PK-EASYOGSDHGLVPRNYEGIVNRVTARFGLDASQOIRLEAE-EKLAHLPLAKTVSV 746  
 DB 292 SESNLTGTDHAIWPSNDSNENIKOPAKCFGLDKLDVYIELKALDSTYTIPTPTTY 351  
 QY 747 EELLQ-VYELQDPTVTRTOLRAMAKTVCPHAKVELEALL---EKQAYKEQVLAKRLTML 801  
 DB 352 GAVIRHHLISGVSQOFPLSTAG---FAPDEETKKAFTRLGGDKQFAKVRKKNFNTA 408  
 QY 802 ELL---EKYPACEMKSEFIALPSIRPRYSISSPRVDEKQASITVSVSGEAMSGY 857  
 DB 409 DALLYSNNAWPSDVPFEFLIENVPHLTPRYSSISS-SISEKQLINVTVAVEAEADG 467  
 QY 858 GEYKGIASNYIAELQ-----EGDTITCFISRP-----OSEFTLPDPER 896  
 DB 468 RPYTGAVTNLKNVEIYQNTGKRPVHYDLSGPRGKFNKFLPVHRRSNFTLPKNSST 527  
 QY 897 PLIMVPGTGVAPFRGFVQARKQLEKQOSLGEAHLFYGCRSPHEDYLOEE-LENAQSE 955  
 DB 528 PVLILPGTGVAPLRFVAREVQOVKNGVNGKTLFLYGCGRNSNEDFLYKQMAEYASVL 587  
 QY 956 G-IITLHTAISRPNQPKTYVOHVMEDGKKLIELLDQAHFYICDGSQMAPAVEATLM 1014  
 DB 588 GENFEMFNASRQDPSKRYVODKILENSQLVHELLTEGAILIYCCDASARMADVQTTIS 647  
 QY 1015 KSYADVHOVSEADARLMLQOLEKGRYAKDVW 1046  
 DB 648 KIVAKSREISEDKAELVXSMKVONRYQEDVW 679

RESULT 15  
 US-10-138-905-83  
 Publication No. US20030068800A1  
 GENERAL INFORMATION:  
 APPLICANT: Wilson, Ron C.  
 APPLICANT: Craft, David L.  
 APPLICANT: Birch, Dudley  
 APPLICANT: Eshoo, Mark  
 APPLICANT: Madduri, Krishna M.  
 APPLICANT: Cornett, Cathy A.  
 APPLICANT: Brenner, Alfred A.

APPLICANT: Tang, Maria  
 APPLICANT: Lopez, John C.  
 APPLICANT: Gleeson, Martin  
 TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME  
 TITLE OF INVENTION: P450 OXIDOREDUCTASE  
 TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C  
 TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO  
 FILE REFERENCE: 1010-16  
 CURRENT APPLICATION NUMBER: US/10/138,905  
 CURRENT FILING DATE: 2002-05-03  
 PRIOR APPLICATION NUMBER: US/09/976,800  
 PRIOR FILING DATE: 2001-10-12  
 NUMBER OF SEQ ID NOS: 118  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 83  
 LENGTH: 679  
 TYPE: PRT  
 ORGANISM: CANDIDATROPICALIS  
 US-10-138-905-83

Query Match 10.9%; Score 597; DB 9; Length 679;  
 Best Local Similarity 27.2%; Pred. No. 2,1e-35;  
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

QY 430 ELDIKETTLKPGFVVKAKSKKI---PLGGIPSPSTEOSAKVKRKAENAHNTPLVL 485  
 DB 5 KDLVYIITLVVAAYFAKNOFLDQPODPTGFLNTDGSNSRDVLLTLKKNKNT--LLL 62  
 QY 486 YGSNMGTAEGTADLADIAMSK-GFAPQVATLDH---AGNLPREGAVLITVASY-NGH 539  
 DB 63 FSGQTAEADYANKLSRELHSRGLTMTVADPADYMDNFGDITEDILVFIATYGEGE 122  
 QY 540 PPNNAQOFVMDLQDASADEVKGVRYSVFGGDKMATTYOKVPAF---IDETLAAGAEN 596  
 DB 123 PTNMADEFTWLTE-EADTLSTLKTIVFGLGN---STIEFFNAIGRKPRLLSEKGD 177  
 QY 597 IADRGADASDDEGTVEE---WREHMSDVAAYFNLD----- 631  
 DB 178 FAEYAE---GDDGTGLTDEDFPMAMKDNVPALKNDLNFEKEKLYEPNVKLTERRDL 234  
 QY 632 ---IENSDNKSTLSIQFVDSAADMPLAKHGAFTNVVASKELQPGSARSTRHLEIEL 688  
 DB 235 DSGVSLGEPNKKYINSBGIDLTGK-PFDHHT-PLYARITETRELFS-SKDRHCIHVEFDI 291  
 QY 689 PK-EASYOGSDHGLVPRNYEGIVNRVTARFGLDASQOIRLEAE-EKLAHLPLAKTVSV 746  
 DB 292 SESNLTGTDHAIWPSNDSNENIKOPAKCFGLDKLDVYIELKALDSTYTIPTPTTY 351  
 QY 747 EELLQ-VYELQDPTVTRTOLRAMAKTVCPHAKVELEALL---EKQAYKEQVLAKRLTML 801  
 DB 352 GAVIRHHLISGVSQOFPLSTAG---FAPDEETKKAFTRLGGDKQFAKVRKKNFNTA 408  
 QY 802 ELL---EKYPACEMKSEFIALPSIRPRYSISSPRVDEKQASITVSVSGEAMSGY 857  
 DB 409 DALLYSNNAWPSDVPFEFLIENVPHLTPRYSSISS-SISEKQLINVTVAVEAEADG 467  
 QY 858 GEYKGIASNYIAELQ-----EGDTITCFISRP-----OSEFTLPDPER 896  
 DB 468 RPYTGAVTNLKNVEIYQNTGKRPVHYDLSGPRGKFNKFLPVHRRSNFTLPKNSST 527  
 QY 897 PLIMVPGTGVAPFRGFVQARKQLEKQOSLGEAHLFYGCRSPHEDYLOEE-LENAQSE 955  
 DB 528 PVLILPGTGVAPLRFVAREVQOVKNGVNGKTLFLYGCGRNSNEDFLYKQMAEYASVL 587  
 QY 956 G-IITLHTAISRPNQPKTYVOHVMEDGKKLIELLDQAHFYICDGSQMAPAVEATLM 1014  
 DB 588 GENFEMFNASRQDPSKRYVODKILENSQLVHELLTEGAILIYCCDASARMADVQTTIS 647  
 QY 1015 KSYADVHOVSEADARLMLQOLEKGRYAKDVW 1046  
 DB 648 KIVAKSREISEDKAELVXSMKVONRYQEDVW 679



Fri May 30 09:30:21 2003

us-10-031-241-35.rapb

Page 10

Search completed: May 29, 2003, 10:15:53  
Job time : 57 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:01:53 ; Search time 48 Seconds

(without alignments)  
2098.935 Million cell updates/sec

Title: US-10-031-241-35

Perfect score: 5457  
Sequence: 1 TIKEMPOKTFEGELKPLPL.....RLMLQOLEEKGRYAKDWMAG 1048

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_73:\*\*\*  
2: p1r1:\*\*\*  
3: p1r2:\*\*\*  
4: p1r3:\*\*\*  
5: p1r4:\*\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5457	100.0	1049	1 A34286	NADPH-ferrihemopro
2	3314	60.7	1061	2 D69799	cytochrome P450 /
3	3281.5	106.1	1054	1 A69975	NADPH-ferrihemopro
4	777.5	14.2	678	1 RDRT04	NADPH-ferrihemopro
5	769	14.1	677	1 RDPG04	NADPH-ferrihemopro
6	769	14.1	679	2 A25505	NADPH-ferrihemopro
7	767	14.1	677	2 A60557	NADPH-ferrihemopro
8	761.5	14.0	678	2 S27158	NADPH-ferrihemopro
9	739.5	13.6	692	2 T05582	NADPH-ferrihemopro
10	737.5	13.5	681	2 T14993	NADPH-ferrihemopro
11	735.5	13.5	671	2 A56592	NADPH-ferrihemopro
12	723	13.2	601	2 A28577	NADPH-ferrihemopro
13	723	13.2	630	2 A47298	NADPH-ferrihemopro
14	711.5	13.0	683	2 T10720	NADPH-ferrihemopro
15	711	13.0	692	2 S37159	NADPH-ferrihemopro
16	709	13.0	711	2 T14081	NADPH-ferrihemopro
17	706	12.9	705	2 T10723	NADPH-ferrihemopro
18	705.5	12.9	590	2 S37157	NADPH-ferrihemopro
19	705	12.9	699	2 T14904	NADPH-ferrihemopro
20	702.5	12.9	712	2 S21531	NADPH-ferrihemopro
21	702	12.9	714	1 S31502	NADPH-ferrihemopro
22	684.5	12.5	662	2 C88451	protein K10D2.6 [1
23	683.5	12.5	1147	1 I56575	nitric-oxide synth
24	679	12.4	1429	2 JN0609	nitric-oxide synth
25	678	12.4	1429	2 S16233	nitric-oxide synth
26	675.5	12.4	1147	1 S38253	nitric-oxide synth
27	675.5	12.4	1147	1 I53165	nitric-oxide synth
28	675.5	12.4	1147	1 JCS029	nitric-oxide synth
29	675	12.4	1433	2 G01946	nitric-oxide synth

30	671.5	12.3	1147	1 S47647	nitric-oxide synth
31	669	12.3	713	2 JE0230	NADPH-cytochrome P
32	665.5	12.2	1144	1 A43271	nitric-oxide synth
33	664.5	12.2	1147	2 JCS028	nitric-oxide synth
34	661	12.1	1153	2 A49676	nitric-oxide synth
35	657.5	12.0	693	1 S38427	NADPH-ferrihemopro
36	654.5	12.0	1147	2 UC5027	nitric-oxide synth
37	654.5	12.0	1147	2 S65440	nitric-oxide synth
38	639	11.7	680	2 S63598	NADPH-ferrihemopro
39	636.5	11.7	607	2 A83726	sulfite reductase
40	628.5	11.5	605	1 G70040	sulfite reductase
41	628	11.5	680	2 S63895	NADPH-ferrihemopro
42	627.5	11.5	506	2 S37156	NADPH-ferrihemopro
43	617.5	11.3	710	2 JC7192	NADPH-ferrihemopro
44	614.5	11.3	1247	2 T31331	nitric-oxide synth
45	608.5	11.2	1203	1 A47501	nitric-oxide synth

#### ALIGNMENTS

##### RESULT 1

A34286 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - *Bacillus megaterium*  
N/Contains: NADPH-ferrihemoprotein reductase (EC 1.6.2.4) ; unspecific monooxygenase (EC 1.10.3.1)  
C/Species: *Bacillus megaterium*  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 03-Jun-2002  
C/Accession: A34286; S43653  
R/Ruettiger, R.T.; Wen, L.P.; Fulco, A.J.  
J. Biol. Chem. 264, 10987-10995, 1989  
A/Title: Coding nucleotide, 5' regulatory, and deduced amino acid sequences of P-450-BM-1  
A/Reference number: A34286; MUID:89291834; PMID:2544578  
A/Accession: A34286  
A/Molecule type: DNA  
A/Residues: 1-1049 <RUE>  
A/Cross-references: GB:04032; MID:9142797; PIDN:AA87602.1; PID:9142798  
R/Munro, A.W.; Lindsey, J.G.; Coggin, J.R.; Kelly, S.M.; Price, N.C.  
FEBS Lett. 343, 70-74, 1994  
A/Title: Structural and enzymological analysis of the interaction of isolated domains of  
A/Reference number: S43653; MUID:94215710; PMID:8163021  
A/Accession: S43653  
A/Molecule type: Protein  
A/Residues: 430-439; 441-496 <MCN>  
C/Genetics:  
A/Gene: CYP102  
C/Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin hom  
C/Keywords: chromoprotein; electron transfer; FAD; flavoprotein; FMN; heme; iron; metallo  
F;262-423/Domain: cytochrome P450 homology <P45>  
F;483-1046/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
F;485-622/Domain: flavodoxin homology <FLX>  
F;401/Binding site: heme iron (Cys) (axial ligand) #status predicted.

Query Match 100.0%; Score 5457; DB 1; Length 1049;  
Best Local Similarity 100.0%; Pred. No. 3.1e-298;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TIKEMPOKTFEGELKPLPLNTDQVQALMKIADGEIKFPAQGVTVRYLSQRIKX	60
DB	2	TIKEMPOKTFEGELKPLPLNTDQVQALMKIADGEIKFPAQGVTVRYLSQRIKX	61
QY	61	ACDESREDFKSLQALKFVRDPADGGLFTSWTHKKNWKAHNLPSFSQAMKGYHAMV	120
DB	62	ACDESREDFKSLQALKFVRDPADGGLFTSWTHKKNWKAHNLPSFSQAMKGYHAMV	121
QY	121	DIIVQVQKWERLNADEHIEVPEDMRLTLDTIGLGCFFNRRNSFYRDQHPPTTSVRA	180
DB	122	DIIVQVQKWERLNADEHIEVPEDMRLTLDTIGLGCFFNRRNSFYRDQHPPTTSVRA	181
QY	181	LDANMKLQKRPANDDPAYDENKQFOEDIKVMDLVDKIIADKASGEOSDDLLTHMLNG	240
DB	182	LDANMKLQKRPANDDPAYDENKQFOEDIKVMDLVDKIIADKASGEOSDDLLTHMLNG	241
QY	241	KDETEGPELDENIRYQIITFLIAGHETTSGLSFALYFLVKNPHYLQKAAEAARVLVD	300

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|||||
242 KDPETGPELDDENIRYOITFLIGHETTSGLTSFALYFLVKNHVLQKAEEARVLVD 301
QY PVPEYKVKOLKYGVMVNEALRLMPTAPASLYAKEDTVYGGVPLEKGEMLVLLPOL 360
Db PVPEYKVKOLKYGVMVNEALRLMPTAPASLYAKEDTVYGGVPLEKGEMLVLLPOL 361
QY HRDRTIMGDDVEEERPERFENPSAIPQAFKPFNGORACIGQOFALHEATLVLMMLKH 420
Db HRDRTIMGDDVEEERPERFENPSAIPQAFKPFNGORACIGQOFALHEATLVLMMLKH 421
QY PDPEFDHNYELDIKETTLTKPEGFVYVAKSKKIPLGIPSTQSAKVKAKKEMANHT 480
Db PDPEFDHNYELDIKETTLTKPEGFVYVAKSKKIPLGIPSTQSAKVKAKKEMANHT 481
QY PLVLVYSGNMGATGARDLADLADIMSKGFAPOVATLDSHAGNLPRBGAVLLVTASYNHP 540
Db PLVLVYSGNMGATGARDLADLADIMSKGFAPOVATLDSHAGNLPRBGAVLLVTASYNHP 541
QY PDNAKQFVMDLQASADEVKGVRSVFGCGDKNNATYQKVPAFIDETLAKGAENIADR 600
Db PDNAKQFVMDLQASADEVKGVRSVFGCGDKNNATYQKVPAFIDETLAKGAENIADR 601
QY PDNAKQFVMDLQASADEVKGVRSVFGCGDKNNATYQKVPAFIDETLAKGAENIADR 601
Db PDNAKQFVMDLQASADEVKGVRSVFGCGDKNNATYQKVPAFIDETLAKGAENIADR 601
QY GEADASDDEFGTYEERHWMMSDVAAVFNLDIENSDNKSTLSIQFVDSAADMLAKMKG 660
Db GEADASDDEFGTYEERHWMMSDVAAVFNLDIENSDNKSTLSIQFVDSAADMLAKMKG 661
QY AFSTNNVASKELQOPGASRSTRHLEIELPKASVOEGDHLVTPRVNGVINYRTARGL 720
Db AFSTNNVASKELQOPGASRSTRHLEIELPKASVOEGDHLVTPRVNGVINYRTARGL 721
QY DASOQIRLEAEERKLAHLPLAKTVSVEELLQYVELQDPVTRTOLRAMAKTVCPHKKEL 780
Db DASOQIRLEAEERKLAHLPLAKTVSVEELLQYVELQDPVTRTOLRAMAKTVCPHKKEL 781
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Db EALLKQAYKEQVLAKRITMLLELKYAPACMKSEFALLIPSTRPRYSISSPRVDEK 841
QY QASTTVSVSGEAMSGVEYGVGASNYVLAELQEGDTTCFTSTQSEPTLRKDPPTPLIM 900
Db QASTTVSVSGEAMSGVEYGVGASNYVLAELQEGDTTCFTSTQSEPTLRKDPPTPLIM 901
QY VGPSTGVAPFRFGVQARQKLEQSGSLGEALYFCRSPHEDYLYOELENAQSGITTL 960
Db VGPSTGVAPFRFGVQARQKLEQSGSLGEALYFCRSPHEDYLYOELENAQSGITTL 961
QY HTAFSRMPNQKTYVOHVMEDGKKLIELDQGAHFYICGDSGOMAPAVEATLMKSYADV 1020
Db HTAFSRMPNQKTYVOHVMEDGKKLIELDQGAHFYICGDSGOMAPAVEATLMKSYADV 1021
QY HOVEADARLWLQOLEKGRYAKDVMAG 1048
Db HOVEADARLWLQOLEKGRYAKDVMAG 1049

```

## RESULT 2

D69799  
cytochrome P450 / NADPH-cytochrome P450 r homolog yeto - Bacillus subtilis  
C/Species: Bacillus subtilis  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 28-Jul-2000  
C/Accession: D69799

R/Kunst, F.; Ogasaawa, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.; Bron, S.; Broutillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emerson, P.T.; Eutlian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.  
Nature 390, 249-256, 1997  
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funo, S.; Galizzi, A.; Gall  
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue  
Y, M.; Ogawa, K.; Ogatawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon  
A/Authors: Schleich, S.; Schroeter, R.; Scifone, R.; Sekiguchi, J.; Sekowska, A.; Serod

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K  
A/Authors: Yoshikawa, H.F.; Zumbato, E.; Yoshikawa, H.; Danchin, A.  
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A/Reference number: A69580; MUID:98044033; PMID:9384377  
A/Accession: D69799  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-1061 <RUN>  
A/Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12544.1; PID:g2633038  
A/Experimental source: strain 168  
A/Genetics:  
A/Gene: yeto  
C/Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin hom  
C/Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein  
F:264-425/Domain: cytochrome P450 homology <P45>  
F:493-1057/Domain: NADPH-ferrithemoprotein reductase homology <FEH>  
F:495-632/Domain: Flavodoxin homology <FLX>  
F:403/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 60.7%; Score 3314; DB 2; Length 1061;  
Best local similarity 59.5%; Pred. No. 5, 7e-178;  
Matches 628; Conservative 156; Mismatches 259; Indels 12; Gaps 6;

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QY 5 MPQKTEGELKUNPLNTDKRVOALMKIADLEGIFKEAPGRVTRYLSQRLKACDE 64
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QY 65 SRPKNLSQALKPRDASGGLFTSWTHKQWKAHNLILPSPQOMKGYHAMVNLAV 124
Db 67 ERFDKSLEGALKERASGGLFTSWTHKQWKAHNLILPSPQOMKGYHAMVNLAV 126
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Db 127 QLVQKMERLANDEHEIPEMDNTRLTDTIGLGFENFNSFNSQDPHFTSMVRAUDEA 186
QY 185 MNKLQANPDDPAYDENKROFQEDIKVMDLVKTIADKASGEQSD-DLITMLNKDP 243
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Db 247 ETGPELDDENIRYOITFLIGHETTSGLTSFALYFLVKNHVLQKAEEARVLVDVP 306
QY 304 SYKQVKQLKYGVMVNEALRLMPTAPASLYAKEDTVYGGVPLEKGEMLVLLPOLHRD 363
Db 307 TYKQVLELYIRMLNSLRMLMPTAPASLYAKEDTVYGGVPLEKGEMLVLLPOLHRD 366
QY 364 KTIWGDVEEERPERFENPSAIPQAFKPFNGORACIGQOFALHEATLVLMMLKHDF 423
Db 367 RDAGKDAEERPERFENPSAIPQAFKPFNGORACIGQOFALHEATLVLMMLKHDF 426
QY 424 EDHNYELDIKETTLTKPEGFVYVAKSKKIPLGIPSTQSAKVKAKKEMANHT 477
Db 427 IDHNYELDIKETTLTKPEGFVYVAKSKKIPLGIPSTQSAKVKAKKEMANHT 480
QY 478 --HNTPLLVYSGNMGATGARDLADLADIMSKGFAPOVATLDSHAGNLPRBGAVLLVTAS 535
Db 487 GLNRPPLLVYSGNMGATGARDLADLADIMSKGFAPOVATLDSHAGNLPRBGAVLLVTAS 546
QY 536 YNGHPDNNAKQFVMDLQASADEVKGVRSVFGCGDKNNATYQKVPAFIDETLAKGA 595
Db 547 YNGHPDNNAKQFVMDLQASADEVKGVRSVFGCGDKNNATYQKVPAFIDETLAKGA 606
QY 596 NIARGEADSDDEFGTYEERHWMMSDVAAVFNLDIENSDNKSTLSIQFVDSAADMP 654
Db 607 RFSARGGDSVDEGQLEKKSMAWDAIKAFLEINENADKRSSTLSIQFVGLGESP 666
QY 655 LAKHGAFTTVVASKELQOPGASRSTRHLEIELPKASVOEGDHLVTPRVNGVINYRV 714
Db 667 LAKHGAFTTVVASKELQOPGASRSTRHLEIELPKASVOEGDHLVTPRVNGVINYRV 726
QY 715 TARPGLDASOQIRLEAEERKLAHLPLAKTVSVEELLQY-VELQDPVTRTOLRAMAKTV 773

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QY 780 LEALAE-----KQAYKEOVLAKLTLMLLEKYPACEMKESFIALPLSIRPRYSISS 834  
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 QY 835 PRVDEKQASTTVVSGEAMSGYGEYKGIASNTYL-AELOEGDT-----ITCFISTPOSEF 888  
 Db 461 SKHAPNSVHLCVAVVEYETKSGGVN-KGVATSWLRKAPAGENGRRALVPMFVR--KSGF 517  
 QY 889 TLKDEPPLIMVGPVGVA--PPGFVQARKOLKEOGSLGEAMHLYECSRPHEDYLYQEE 948  
 Db 518 RLFPFKATTPVIMVGPVGVA--PPGFVQARKOLKEOGSLGEAMHLYECSRPHEDYLYQEE 577  
 QY 949 LENAQSEGIT-LHTAFSRMPNQP-KTYVQVHMEODGSKLIELT-DOGAHFIYICGDSQOM 1005  
 Db 578 LAQFHAAGALTRLSVANSR--EQQKAYVQHLKRDKEHMLKIHOGCAHIIYICGDARNM 635  
 QY 1006 APVAVETLMKSYADVHOVSADARLMLQOLEEKGRVAKDYVA 1047  
 Db 636 ARDVONTFCDIVAEOGFMEHAQADVYKCLMTKGRVSLDWMS 677

## RESULT 6

A25505  
 NADPH-ferrithemoprotein reductase (EC 1.6.2.4) - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 05-Oct-1988 #sequence\_revision 05-Oct-1988 #text\_change 03-Jun-2002  
 C/Accession: A25505; A05233  
 R/Katagiri, M.; Murakami, H.; Yabusaaki, Y.; Sugiyama, T.; Okamoto, M.; Yamano, T.; Ohkaw  
 J.; Biochem. 100, 945-954, 1986  
 A>Title: Molecular cloning and sequence analysis of full-length cDNA for rabbit liver NA  
 A/Reference number: A25505; MUID:87137361; PMID:3029050  
 A/Accession: A25505  
 A/Molecule type: mRNA  
 A/Residues: 1679 <KAT>  
 A/Cross-references: GB:X04610; NID:91543; PIDN:CAA28279.1; PID:91544  
 R/Black, S.D.; Coon, M.J.  
 J. Biol. Chem. 257, 5929-5938, 1982  
 A>Title: Structural features of liver microsomal NADPH-cytochrome P-450 reductase. Hydric  
 A/Reference number: A05233; MUID:82167456; PMID:6802823  
 A/Accession: A05233  
 A/Molecule type: protein  
 A/Residues: PTHGG, 14-39, 'NY', 42-52, 'N', 54-81 <BLA>  
 A/Note: the order of the first four residues was not determined  
 A/Note: the amino end of the mature protein is acetylated  
 C/Comment: This enzyme, a membrane-bound flavoprotein containing one molecule each of FM  
 C/Superfamily: NADPH-ferrithemoprotein reductase; Flavodoxin homology; NADPH-ferrithemoprot  
 C/Keywords: acetylated amino end; electron transfer; FAD; Flavoprotein; FMN; membrane pr  
 F/1-56/Domain: membrane-bound #status predicted <MEM>  
 F/78-228/Domain: FMN binding #status predicted <MEM>  
 F/81-677/Domain: NADPH-ferrithemoprotein reductase homology <FEH>  
 F/83-225/Domain: flavodoxin homology <FLX>  
 F/85-96/Region: FMN-phosphate binding #status predicted  
 F/268-327/453-478/Domain: FAD binding #status predicted <FAD>  
 F/294-297/Region: FAD-pyrophosphate binding #status predicted

Query Match 14.1%; Score 769; DB 2; Length 679;  
 Best Local Similarity 31.7%; Pred. No. 1.9e-35;

Matches 212; Conservative 111; Mismatches 250; Indels 96; Gaps 24;

QY 444 FVYAKSKKIP-----LGIPIPSPTQGA--KAYRKKANANHTPLVLYGNNMGTAEGTA 497  
 Db 42 FLPRKKKEVEBPTKIQAPRSSVYKSSFVEKKKKTKRNN-----IVFYGSSQGTAEFA 96  
 QY 498 RDLADLAMSNGFAPQVATLDSH-----AGNIPREGAVILV--TASY-NGHPDPAKQFVW 550  
 Db 97 NRTLSKQAHRYGKMGMAADPEEYDLADLSLPEINNALAVCMATYGGEDPTDAAQFYDW 156  
 QY 551 LDOASADEVGVRSYVFGCDKXWATTYQKVA---FIDEFLAKAGENIADGENDASD 607  
 Db 157 LQETDWD-LSGVKAIVAGLGAK--TYEFNNMGKTVDRLEQLGQRIFEIAGMDDDA 211  
 QY 608 DFEQTYEWEHMHMSDVAAAYFNLDIENSEDNKSTLSLQFVDSADAMELATQH----- 659

Db 212 NLEDEFTWREQFWPAVCEHFGEATGEESIRQVELVL---HTDIDVAKVYOGEMGRK 268  
 QY 660 -----GAFSTNVASKELELOPGSARSTRLEIEL-PKENSYOGCDILGYIPRN 706  
 Db 269 SYENQKPPDANKPFLATVYTNKLNQ-GTERLMLHELDI SDSKIRYESGDVAAVY PAN 327  
 QY 707 YEGIVARVTARFGLDASQCI---RLBAEEKLAHLPL-----AKTVSV 746  
 Db 328 DSAVLVNOQLEILGADLDVWMSLNNDLESKNGKHPFCPSYRTALTYIDITNPPRTNV 387  
 QY 747 EBLQYVELQDPVTRTQLRMAAKTVCPPHKVELLEALKQAYKEOVLAKRLTMLLELEK 806  
 Db 388 YELAQVA--ADPAEQQLRKMASSSG-----EGKELYLSWVEARRHILALLOD 434  
 QY 807 YPACEMKESFIALPLSIRPRYSISSPRVDEKQASITVSVSGEAMSGYGEYKGIASN 866  
 Db 435 YPSLRPPIDHLCCELLRLQARRYSIASSSKVPHNSVHICAVAVEYETKAGRLN-KGVATS 493  
 QY 867 YL-AELOEGDT-----ITCFISTPOSEFTLPKDPETPLIMVGPVGVA--PPGFVQARKOL 920  
 Db 494 WLRKAPAGENGRRALVPMFVR--KGFRLPFAATTPVIMVGPVGVA--PPGFVQARKOL 551  
 QY 921 KEQGSGLGEAHLYEGCRSPHEDYLYOELENAQSEGIT-LHTAFSRMPNQPRTYVQVHM 979  
 Db 552 ROQKEVGETILYYGCRRAEDLYAREELAGFQKDGTLSQLNVAFSREGAO-KVYVQHL 610  
 QY 980 EDOGKULIELDD-GAHFIYICGDSQOMAPVAVETLMKSYADVHOVSADARLMLQOLEEK 1038  
 Db 611 RRKEHMLRLIHGGAHIVYCGDARNVADVONTFYDIVAELGAMHAQADVYKCLMTK 670  
 QY 1039 GRVAKDYVA 1047  
 Db 671 GRVSLDWMS 679

## RESULT 7

A60557  
 NADPH-ferrithemoprotein reductase (EC 1.6.2.4) - human  
 N/Alternate names: NADP-cytochrome P450 reductase  
 C/Species: Homo sapiens (man)  
 C/Date: 17-Apr-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-Jun-2002  
 C/Accession: A33421; A60557; S21686  
 R/Hanin, M.; McMahon, M.E.; Birkett, D.J.; Lee, T.D.; Shively, J.E.  
 Biochemistry 28, 8639-8645, 1989  
 A>Title: Structural and functional analysis of NADPH-cytochrome P-450 reductase from hu  
 A/Reference number: A33421; MUID:90105350; PMID:2513880  
 A/Accession: A33421  
 A/Molecule type: protein  
 A/Residues: 2-677 <HAN>  
 A/Note: 551-Gln was also found  
 R/Yamano, S.; Aoyama, T.; McBride, O.W.; Hardwick, J.P.; Gelboin, H.V.; Gonzalez, F.J.  
 Mol. Pharmacol. 36, 83-88, 1989  
 A>Title: Human NADPH-P450 oxidoreductase: complementary DNA cloning, sequence and vaccin  
 A/Reference number: A60557; MUID:89313720; PMID:2501655  
 A/Accession: A60557  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-137, 'G', 139-577, 'DV', 580-677 <YAN>  
 R/Shephard, E.A.; Palmer, C.N.A.; Segall, H.J.; Phillips, I.R.  
 Arch. Biochem. Biophys. 294, 168-172, 1992  
 A>Title: Quantification of cytochrome P450 reductase gene expression in human tissues.  
 A/Reference number: S21686; MUID:92198003; PMID:1550342  
 A/Accession: S21686  
 A/Molecule type: mRNA  
 A/Residues: 2-499, 'V', 501-517, 'L', 519-536, 'WH', 539-677 <SHE>  
 A/Cross-references: GB:S90469; NID:9247306; PIDN:AA81814.1; PID:9247307  
 C/Superfamily: NADPH-ferrithemoprotein reductase; Flavodoxin homology; NADPH-ferrithemoprot  
 C/Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; Flavoprc  
 F/1-56/Domain: membrane-bound #status predicted <MEM>  
 F/2-677/Product: NADPH-ferrithemoprotein reductase #status experimental <MAT>  
 F/77-227/Domain: FMN binding #status predicted <FNU>  
 F/80-675/Domain: NADPH-ferrithemoprotein reductase homology <FEH>

F:82-224/Domain: flavodoxin homology <FLX>  
 F:84-95/Region: FMN-phosphate binding #status predicted <FAD>  
 F:267-326,452-477/Domain: FAD binding #status predicted <FAD>  
 F:293-286/Region: FAD-pyrophosphate binding #status predicted  
 F:2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental  
 F:566/Binding site: NADP (Cys) #status experimental

Query Match 14.1%; Score 767; DB 2; Length 677;  
 Best Local Similarity 32.4%; Pred. No. 2,56-35;  
 Matches 211; Conservative 113; Mismatches 264; Indels 64; Gaps 23;

QY 444 FVYAKSKKIP-----LGIPTSPSTEQS-AKVYKKAENAHNTPLLYGSMGTAEGRAR 498  
 DB 42 FLFRKKKEEVEFTKISTTTSSVKESSFVEMKKTGRN-----IIFYGQGTAEERFAN 96  
 QY 499 DLADIAMSKGAPAVATLDH-----AGNLPREGAVLY--TASY-NGHPPNKAQFVDWL 551  
 DB 97 RLSDKHARHYGMKGMAADPEEYDLADLSLPEIDNALVFCMATYGEQDPTNADQFYDWL 156  
 QY 552 DQASADVKYRVSVFGCGDKMATTYQKVPAR---FIDETLAAGAENIADREASDSD 608  
 DB 157 QETDVL-DLSGVKAVFGLGNK---TYEHFAMGKYVDKRLQGLGAQRIFELGLGDDGN 211  
 QY 609 FEGTYEEMREHMSDVAAYFNLDIENSNDKSTLSLOF---VDSA---ADMLAKMH-- 659  
 DB 212 LEBDFITWREQFWPVCHEFVEATGEBSIRQYELVHTDIDAKVYMGEMGRKSYEN 271  
 QY 660 -----GAFSTNVASKELOQPGSARSTRHLEIEL-PKEASYOEQDHLGVIIRYEGI 710  
 DB 272 QKPPFDANKPFLAAVTTNRKLNQ-GTERHLMHLELDISDKIRYESGDHVAVYPANDSNL 330  
 QY 711 VNRVTARFG--LDASQOIRLEAEBEKLAHLPLAKTVSEVLLQYVELQDPTVTRQLRAMA 768  
 DB 331 VNQGLKIGADLDVMSLNINDESNKKGPPCPPTSYRTALTYLDINP-PRTNVLYEL 389  
 QY 769 AKTYCPRHKEVLEALLF-----KQAYKEQVLAKRLTMLELLEKYPACEKMFSEFIALP 822  
 DB 390 AQVASESEBQELHKKMASSGEGKELYLVWVEARHILAILODCPSPRPIDHLCETLP 449  
 QY 823 SIRRYYSISSPRVDEKQASITVSVSGEAMSGYGEYKGIASNYL-AELOEGDT----- 876  
 DB 450 RLQARYSIASSKVNHSVHICAVVVEYETKGRIN-KGVAITMWRKPEAPENGRRAL 508  
 QY 877 ITCEISTPOSEFTLPKDPETPLIMVPGTGVAPFRGVQARKOLKEGOSLGEAHLYFGC 936  
 DB 509 VPMFVR--KSQFRLPFKATTPVIMVGGTGVAPFIFGIQERAWLQOQKEVGETLLTYGC 566  
 QY 937 RSPHEDLYOELENAQSEGIIT-LHTAFSRMNPQPTVYQVHMEODGKLIIELDQGAH 995  
 DB 567 RRSDEDLVREELAQFHRDGLTQLNVAFSREOSH-KYVVOHLKODREHMLKULEGGAH 625  
 QY 996 FYICGDSQMAPAVEATLMKSYADVHOVSEADARLMLQOLEKGRYAKDVMA 1047  
 DB 626 IYVCGDARNMARVDQNTFYDIAELGMEHQAQVDYIKKLMTKGRISLDVMS 677

# RESULT 8

S27158  
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - guinea pig  
 N:Alternate names: NADPH-cytochrome P450 oxidoreductase  
 C:Species: *Cavia porcellus* (guinea pig)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 03-Jun-2002  
 C:Accession: S27158; #sequence\_revision 03-Feb-1994  
 R:Obtainer: S. J. Goda, T. J. Ishizaki, K. J. Kametaki, T. J. Shniriki, N. Blochlin, Biophys. Acta 1171, 103-105, 1992  
 A:Title: Molecular cloning and sequence analysis of mouse NADPH-cytochrome P-450 oxidoreductase  
 A:Reference number: S27158; MUID:93041995; PMID:1420354  
 A:Accession: S27158  
 A:Molecule type: mRNA  
 A:Residues: 1-678 <OHG>  
 A:Cross-references: EMBL:D10498; NID:q220556; PIDN:BA01385.1; PID:q220557  
 A:Note: the species identification has been revised in reference S38510  
 R:Obtainer: S. J. Goda, T. J. Ishizaki, K. J. Kametaki, T. J. Shniriki, N.

Biochim. Biophys. Acta 1174, 313, 1993  
 A:Reference number: S38510; MUID:93385164; PMID:8373812  
 A:Contents: annotation: erratum  
 C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase; electron transfer; endoplasmic reticulum; FAD; flavoprotein; FMN; NADP; oxidoreductase  
 F:80-676/Domain: NADPH-ferrihemoprotein reductase homology <FEH>  
 F:82-224/Domain: flavodoxin homology <FLX>  
 F:292-326,454-477/Domain: FAD binding #status predicted <FAD>

Query Match 14.0%; Score 761.5; DB 2; Length 678;  
 Best Local Similarity 31.9%; Pred. No. 56-35;  
 Matches 208; Conservative 111; Mismatches 269; Indels 65; Gaps 22;

QY 444 FVYAKSKKIP-----LGIPTSPSTEQS-AKVYKKAENAHNTPLLYGSMGTAEGRAR 498  
 DB 42 FLFRKKKEEVEFTKISTTTSSVKESSFVEMKKTGRN-----IIFYGQGTAEERFAN 96  
 QY 499 DLADIAMSKGAPAVATLDH-----AGNLPREGAVLY--TASY-NGHPPNKAQFVDWL 551  
 DB 97 RLSDKHARHYGMKGMAADPEEYDLADLSLPEIDNSLAVFCMATYGEQDPTNADQFYDWL 156  
 QY 552 DQASADVKYRVSVFGCGDKMATTYQKVPARIDETLAAGAENIADREASDSDFE 611  
 DB 157 QETDVL-DLSGVKAVFGLGNKTY-EHNSMGKYVDKRLQGLGAQRIFELGLGDDGNLE 214  
 QY 612 TYEEMREHMSDVAAYFNLDIENSNDKSTLSLOFVDSADMLAKMH----- 659  
 DB 215 DFTITWREQFWPVCHEFVEATGEBSIRQYELV---HADTPAKVYTEMGRKSYEN 271  
 QY 660 -----GAFSTNVASKELOQPGSARSTRHLEIEL-PKEASYOEQDHLGVIIRYEGI 710  
 DB 272 QKPPFDANKPFLAAVTTNRKLNQ-GTERHLMHLELDISDKIRYESGDHVAVYPANDSNL 330  
 QY 711 VNRVTARFG--LDASQOIRLEAEBEKLAHLPLAKTVSEVLLQYVELQDPTVTRQLRAMA 768  
 DB 331 VNQGLKIGADLDVMSLNINDESNKKGPPCPPTSYRTALTYLDINP-PRTNVLYEL 389  
 QY 769 AKTYCPR-----HKEVLEALLFQAYKEQVLAKRLTMLELLEKYPACEKMFSEFIALP 822  
 DB 390 AQVASESEBQELHKKMASSGEGKELYLVWVEARHILAILODYPSLRPIDHLCETLP 449  
 QY 823 SIRRYYSISSPRVDEKQASITVSVSGEAMSGYGEYKGIASNYL-AELOEGDT----- 876  
 DB 450 RLQARYSIASSKVNHSVHICAVVVEYETKGRIN-KGVAITMWRKPEAPENGRRAL 508  
 QY 877 ITCEISTPOSEFTLPKDPETPLIMVPGTGVAPFRGVQARKOLKEGOSLGEAHLYFGC 936  
 DB 509 VPMFVR--KSQFRLPFKATTPVIMVGGTGVAPFIFGIQERAWLQOQKEVGETLLTYGC 566  
 QY 937 RSPHEDLYOELENAQSEGIIT-LHTAFSRMNPQPTVYQVHMEODGKLIIELDQGA 994  
 DB 567 RRSDEDLVREELAQFHRDGLTQLNVAFSREQAQ-KYVVOHLKODREHMLKULEHEDGA 625  
 QY 995 HFYICGDSQMAPAVEATLMKSYADVHOVSEADARLMLQOLEKGRYAKDVMA 1047  
 DB 626 HIYVCGDARNMARVDQNTFCNIAELGMEHTQAVDYVKKLMTKGRISLDVMS 678

# RESULT 9

T05582  
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) ATR1 - Arabidopsis thaliana  
 N:Alternate names: protein P22K18.280  
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Jun-2002  
 C:Accession: T05582; S21530  
 R:Bevan, M., Wedler, H., Wedler, E., Wambut, R., Hohnsels, J., Mewes, H.W., Mayer, K.F.J. submitted to the Protein Sequence Database, February 1999  
 A:Reference number: 215419  
 A:Accession: T05582  
 A:Molecule type: DNA  
 A:Residues: 1-692 <BEV>  
 A:Cross-references: EMBL:AL035356









submitted to the EMBL Data Library, September 1993

A:Description: Isolation and characterization of a cDNA encoding an NADPH-cytochrome P450

A:Reference number: 537159

A:Accession: 537159

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-692 <BEN>

A:Cross-references: EMBL:Z26252; NID:9400531; PIDN:CA081211.1; PID:9400532

C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoproc

C:Keywords: flavoprotein; NADP; oxidoreductase

F:83-691/Domain: NADPH-ferrihemoprotein reductase homology <FEH>

F:85-234/Domain: flavodoxin homology <FLX>

Query Match 13.0%; Score 711; DB 2; Length 692;

Best Local Similarity 28.4%; Pred. No. 3.5e-32;

Matches 198; Conservative 120; Mismatches 287; Indels 92; Gaps 21;

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QY 406 ALHEATVLVGMMLKHPDEHDHNYELDIKETLTLKPEGFVYKAKSKIPLOGIPSPSTEQ 465
DB 32 ATTSAAVILGLV--FLWRKSPDRSRRLRPVLPK--FTVKHEDDEV----- 76
QY 466 SAKYRKKAENAHNTPLVLVYGSNNGTAEGRADLAD--IAMSQFAPQVATLDSHA--- 520
DB 77 -----DRGKTKVTFYGTGTAEGRFKAALAEIKARYEKAVKVVMDMDYALD 126
QY 521 ----GNLPREGAVLIVTASY-NGHPPDNAQFVMDLQASADE--VKGVRSYVFGGDK 572
DB 127 DQYEKLEKTELVPFMALATYGDGPTDPAARFYKFTGKEERGTLQQLTYGVFALGNR 186
QY 573 NWATTYQVPAFIDETLAKAENIADRGADASDDEFTYEEWREHMSDVAAYFNLDI 632
DB 187 QY-EHFNKIGKIVDEDLTEGAKRLVPVGLDDQSDIEDFNAMKETLMPELD---QL 240
QY 633 ENSEDNKSTLSLQFVDSAADMPLA-----KMGAFSTNVAS 669
DB 241 LRDDDDVNTASTPYTAISEYRVVHDPVSPSYENHFNANGAVFDIHPCRVNAVR 300
QY 670 KELQPGSARSTRHLELP-KEASVQEGDHLGVIPRYEGIVNRVTARFGLDASQIRL 728
DB 301 RELHKPQSDRSCIHFEFLSGTGYETGDHGVYAENCDVEEAGKLGOSLDLFLSL 360
QY 729 EAEERKLAHL-----PLAKTVSVEELLQ-YVELQDPVTRTQLRMAAKTVCPHKVELE 781
DB 361 HTDKEDGSLGSLPPPGPCVTRTALACYADLINPPRKAIVALAHASEPSEAEERLK 420
QY 782 ALLE---KQAYKEQVLAKRLTMLELLEKYPACEMKFSSEFI-ALPSTIRRYSTSSPRV 837
DB 421 FLSSPQGDYSKMWVGSQRLLEVMAFSAKPPPLGVFPALIAIRLQPRYYSISSSPR 480
QY 838 DEKQASITVSVSGEAMSGVEYKGIASNYLAEL---QEGDTITCFISTPQSEFTLPKD 893
DB 481 APQKVHVTICALVEGPTPG-RHKGVCSVTWMSATPLEKSHDCSRAPFIFIRPSNFKLPAD 539
QY 894 PETPLINVGPGTGAFFRGFVQARKQKQKQSGSLGEAHLVFGCRSPHEDVLYQEELENAQ 953
DB 540 HSIRIINVGPGTGLAFFRGFLOERLALKEDEVQGLPALLPFCRRNQMDFIYEDLINNV 599
QY 954 SEGIIIT-LHTAFSPMPNQPKTYVQVHMEQDGKLLIELDQGAHFYICGDSQMAPAVEAT 1012
DB 600 QQGAISELIVAFSR-EGPEKEIVQHKMDKAEVLSLISGGYLVCGDAKGMADVARS 658
QY 1013 LMSYADVHVQVSEAD---ARLMLQOLEKGRYAKDWM 1046
DB 659 L---HTIVQOQENADSSKAEATVKKLQMDGRIYLRDWM 692
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Searched completed: May 29, 2003, 10:07:19  
Job time : 51 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 09:55:08 ; Search time 25 Seconds  
(Without alignments)  
1738.688 Million cell updates/sec

Title: US-10-031-241-35

Perfect score: 5457  
Sequence: 1 TTKEMPOKPTFGELKNLPLL.....RLMLQQLBEKGRYAKDVWAG 1048

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	5457	100.0	1048	1	CPXB_BACME
2	3314	60.7	1061	1	CYPD_BACSU
3	3281.5	60.1	1054	1	CYPE_BACSU
4	778.5	14.3	677	1	NCPR_MOUSE
5	777.5	14.2	677	1	NCPR_RAT
6	769	14.1	677	1	NCPR_PIG
7	769	14.1	679	1	NCPR_RABIT
8	767	14.1	676	1	NCPR_HUMAN
9	761.5	14.0	677	1	NCPR_CAVPO
10	735.5	13.5	671	1	NCPR_MUSDO
11	725.5	13.3	679	1	NCPR_DROME
12	723	13.2	601	1	NCPR_SALT
13	721	13.2	690	1	NCPR_PHAUS
14	702	12.9	714	1	NCPR_CATRO
15	679.5	12.5	1147	1	NOS2_RAT
16	679	12.4	1429	1	NOS1_MOUSE
17	678	12.4	1439	1	NOS1_RAT
18	675	12.4	1434	1	NOS1_HUMAN
19	671.5	12.3	1147	1	NS2D_HUMAN
20	665.5	12.2	1144	1	NOS2_MOUSE
21	662	12.1	1435	1	NOS1_RABIT
22	661	12.1	1153	1	NS2A_HUMAN
23	655	12.0	1136	1	NOS2_CHICK
24	651.5	11.9	1149	1	NOS2_CAVPO
25	642	11.7	1174	1	NOS1_RHOPR
26	639	11.7	680	1	NCPR_CARMA
27	614.5	11.3	1247	1	NOS1_ANOST
28	608.5	11.2	1202	1	NOS3_HUMAN
29	602.5	11.0	1204	1	NOS3_BOVIN
30	594.5	10.9	1201	1	NOS3_MOUSE
31	590.5	10.8	1204	1	NOS3_PIG
32	587	10.8	680	1	NCPR_CANTR
33	564.5	10.3	1350	1	NOS_DROME

34	563	10.3	496	1	NOS2_RABIT	019114	oryctolagus
35	537.5	9.8	678	1	NCPR_SCHPO	P36587	schizosacch
36	534.5	9.8	725	1	MTRR_HUMAN	Q9ub88	homo sapien
37	522	9.6	690	1	NCPR_YEAST	P16603	saccharomyc
38	518.5	9.5	598	1	CYST_ECOLI	P18038	escherichia
39	500.5	9.2	1153	1	NOS1_TYMT	061309	lymaea sta
40	495.5	9.1	598	1	CYST_SALTY	P38039	salmonella
41	488.5	9.0	601	1	CYST_BUCAL	P57503	buchnera ap
42	480.5	8.8	919	1	NOS3_RAT	062600	rattus norv
43	466.5	8.5	682	1	MTMR_CAEEL	017574	caenorhabdi
44	460	8.4	576	1	C927_SOYAN	048921	glycine max
45	459.5	8.4	580	1	C973_ARATH	023365	arabidopsis

## ALIGNMENTS

RESULT 1  
CPXB\_BACME STANDARD; PRT; 1048 AA.  
ID CPXB\_BACME  
AC P14779;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Bifunctional P-450:NADPH-P450 reductase (Cytochrome P450 (BM-3))  
DE (P450BM-3) [Includes: Cytochrome P450 102 (EC 1.14.14.1); NADPH-  
DE cytochrome P450 reductase (EC 1.6.2.4)].  
GN CYP102A1 OR CYP102.  
OS Bacillus megaterium.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1404;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89291834; PubMed=2544578;  
RA Ruettinger R.T., Wen L.-P., Fulco A.J.;  
RT "Coding nucleotide, 5' regulatory, and deduced amino acid sequences  
RT of P-450BM-3, a single peptide cytochrome P-450:NADPH-P-450  
RT reductase from Bacillus megaterium.";  
RL J. Biol. Chem. 264:10987-10995(1989).  
RN [2]  
RP CHARACTERIZATION.  
RX MEDLINE=92088245; PubMed=1727637;  
RA Boddupalli S.S., Pramanik B.C., Slaughter C.A., Estabrook R.W.,  
RA Peterson J.A.;  
RT "Patty acid monooxygenation by P450BM-3: product identification and  
RT proposed mechanisms for the sequential hydroxylation reactions.";  
RL Arch. Biochem. Biophys. 292:20-28(1992).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-471.  
RX MEDLINE=9342510; PubMed=8342039;  
RA Ravichandran K.G., Boddupalli S.S., Hasemann C.A., Peterson J.A.,  
RA Daisenhofer J.;  
RT "Crystal structure of hemoprotein domain of P450BM-3, a prototype for  
RT microsomal P450's.";  
RL Science 261:731-736(1993).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-471.  
RX MEDLINE=97185914; PubMed=9033595;  
RA Li H.Y., Poulos T.L.;  
RT "The structure of the cytochrome P450BM-3 haem domain complexed with  
RT the fatty acid substrate, palmitoleic acid.";  
RL Nat. Struct. Biol. 4:140-146(1997).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.03 ANGSTROMS) OF 1-458 AND 459-649.  
RX MEDLINE=99162523; PubMed=10051560;  
RA Sevrioukova I.F., Li H., Zhang H., Peterson J.A., Poulos T.L.;  
RT "Structure of a cytochrome P450-redox partner electron-transfer  
RT complex.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:1863-1868(1999).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS) OF 1-470.  
RX MEDLINE=21552924; PubMed=11695892;  
RA Haines D.C., Tomchick D.R., Machius M., Peterson J.A.;

RT "Pivotal role of water in the mechanism of P450BM-3.";  
 RL Biochemistry 40:13456-13465(2001).  
 CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. CATALYZES  
 CC HYDROXYLATION OF MEDIUM AND LONG-CHAIN FATTY ACIDS AT OMEGA-1,  
 CC OMEGA-2 AND OMEGA-3 POSITIONS. WITH OPTIMUM CHAIN LENGTHS OF 14-16  
 CC CARBONS (LAURIC, MYRISTIC, AND PALMITIC ACIDS). THE REDUCTASE  
 CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME  
 CC P450.  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferriocytochrome = NADP(+) + 2  
 CC ferriocytochrome.  
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
 CC oxidized flavoprotein + H(2)O.  
 CC -1- COFACTOR: FAD AND FMN.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME  
 CC P450 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 CC EMBL, J04832; AA87602.1; -.  
 DR PIR; A34286; A34286.  
 DR PDB; 2HPD; 3I-OCT-93.  
 DR PDB; 2BMH; 3I-JUL-94.  
 DR PDB; 1FAG; 12-FEB-97.  
 DR PDB; 1FAM; 12-FEB-97.  
 DR PDB; 1BU7; 23-SEP-96.  
 DR PDB; 1BVY; 23-FEB-99.  
 DR PDB; 1JPZ; 09-NOV-01.  
 DR InterPro; IPR001128; Cytochrome P450.  
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 DR InterPro; IPR001709; FPN\_Cyt\_reductase.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00067; P450; 1.  
 DR Pfam; PF00175; NAD binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
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 DB 181 LDEAMNKLQRPNDPPAYDENKROFOEDIKVNDLVYDKIADRKASGEQSDLLTHMLNG 240  
 QY 241 KDPETGEPFLDENIRVOITFLIAGHETTSGLSPALYFLVKNPHTVQKAABEARLVLD 300  
 DB 241 KDPETGEPFLDENIRVOITFLIAGHETTSGLSPALYFLVKNPHTVQKAABEARLVLD 300  
 QY 301 PVPSTYKOVKOLKVGMVNLBALRLMTPAPAFSLYAKEDTVLGGSEYPLEKDEMLVLI 360  
 DB 301 PVPSTYKOVKOLKVGMVNLBALRLMTPAPAFSLYAKEDTVLGGSEYPLEKDEMLVLI 360  
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Db 421 FDEEDHTNVELDKETITLTKEGFFVAKAKKIPLGCIPEBPTBQAKKVKRKAENAHNT 480
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Db 1021 HQVSEADARLMLQOLEKGRVAKDVWAG 1048

RESULT 2
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AC 008334;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable bifunctional P-450:NADPH-P450 reductase 1 [Includes:
DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
DE (EC 1.6.2.4)].
GN CYPD OR CYP102A2.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97453479; PubMed=9308178;
RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., lauber J.,
RA Duesterhoeft A., Ehrlich S.D.;
RT "Sequence of the Bacillus subtilis genome region in the vicinity of
RT polymerase sigma factors Sigv and Sigz.";
RL microbiology 143:2939-2943(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogatawara N., Noszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Betero M.G., Bessieres P., Bolotin A., Borchert S.,

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RA Bortiss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell I.B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerot I.F., Cummings N.J., Daniel R.A.,
RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Ertlen K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Frits C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
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RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Kamata D., Kasahara Y., Kleaer-Blanchard M., Klein C.,
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RA Lee S.M., Levine A., Liu H., Maeda S., Manuel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogawa K., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Portolick S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scotone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Takakoshi A., Tanaka T., Terstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viati A., Wambut R., Wedler E., Wedler H., Weitzneger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
CC P450 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferri-cytochrome = NADP(+) + 2
CC ferri-cytochrome.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- COFACTOR: FAD AND FMN (BY SIMILARITY).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE CYTOCHROME
CC P450 FAMILY.
CC
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DR EMBL: D87979; BAA20123.1; -
DR EMBL: 299107; CAB12544.1; -
DR HSSP: P14779; 1JPZ.
DR Subtilisin, BG12871; cypD.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR003097; FAD binding.
DR InterPro: IPR001709; FMN cyc. reductase.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00067; P450; 1.
DR Pfam: PF00175; NAD binding; 1.
DR Pfam: PF00258; Flavodoxin; 1.
DR Pfam: PF00667; FAD binding; 1.
DR PRINTS: PR00371; PFNCR.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
KW Complete proteome.
FT DOMAIN 1 474 CYTOCHROME P450.
FT BINDING 475 1061 NADPH-P-450 REDUCTASE.
FT BINDING 403 403 HEME (BY SIMILARITY).
SQ SEQUENCE 1061 AA; 119467 MW; 7915DACC20578978 CRC64;
Query Match 60.7%; Score 3314; DB 1; Length 1061;

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Beet Local Similarity 59.5%; Pred. No. 7,1e-178; Indels 12; Gaps 6;  
Matches 628; Conservative 156; Mismatches 259;

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Db 1026 QKAYQAVHGTGEQDAQWNLHLODTGMVYAKDVWAG 1060

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RESULT 3
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ID CYPE_BACSU STANDARD; PRT; 1054 AA.
AC 008336;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable bifunctional P-450:NADPH-P450 reductase 2 (Includes:
DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
DE (EC 1.6.2.4)).
GN CYPE OR CYP102A3.
OC Bacillus subtilis.
OX NCBI_TaxID=1423;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97453479; PubMed=9308178;
RA Socorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
RA Duesterhoeft A., Ehrlich S.D.;
RT "Sequence of the Bacillus subtilis genome region in the vicinity of
RT the lev operon reveals two new extracytoplasmic function RNA
RT polymerase sigma factors Sigv and Sigz."
RL Microbiology 143:2939-2943 (1997).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96044033; PubMed=9384377;
RA Kunst F., Ogatawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Britnell S.C., Bron S.,
RA Brouiller S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cumming N.J., Daniel R.A.,
RA Demizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
RA Gilm S.Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasaahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koelter P., Koningsstein G., Krogh S., Kumano M.,
RA Kusita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Patro V., Pohl T.M., Portetelle D., Portwollik S., Prescott A.M.,
RA Priesecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sao T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Seliguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Socorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Takakoshi A., Tanaka T., Terpestra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambut R., Wedler E., Wedler H., Weitenegger T.,
RA Witters P., Wiput A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256 (1997).
-1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
P450 (BY SIMILARITY)
-1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
ferricytochrome.
-1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
oxidized flavoprotein + H(2)O.
-1- COFACTOR: FAD AND FMN (BY SIMILARITY).
-1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
P450 FAMILY.

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DR EMBL; U93874; AAB80867.1; -;  
DR EMBL; Z99117; CAB14658.1; -;  
DR HSSP; P14779; 1JPZ.  
DR Subtilisin; BGI2299; CYPE.  
DR Interpro; IPR001128; Cytochrome\_P450.  
DR Interpro; IPR003097; FAD\_Binding.  
DR Interpro; IPR001709; FPN\_Cyt\_redctase.  
DR Interpro; IPR001226; Flavodoxin.  
DR Interpro; IPR001433; Oxred\_FAD/NAD(P).  
DR Pfam; PF00067; P450; 1.  
DR Pfam; PF00175; NAD\_Binding; 1.  
DR Pfam; PF00258; Flavodoxin; 1.  
DR Pfam; PF00667; FAD\_Binding; 1.  
DR PRINTS; PR00371; FPNCR.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;  
KW Complete proteome.  
FT DOMAIN 1 475 CYTOCHROME P450.  
FT BINDING 403 403 NADPH-P-450 REDUCTASE.  
FT BINDING 403 403 HEME (BY SIMILARITY).  
SQ SEQUENCE 1054 AA; 118675 MW; 705F8E27866CA110 CRC64;

Query Match Best Local Similarity 58.1%; Score 3281.5; DB 1; Length 1054;  
Matches 614; Conservative 173; Mismatches 254; Indels 9; Gaps 6;

QY 5 MPQRTFGEIKNPLPLNTDKPVQALMKIADLGEIPEKFAEGRVTRYLSORLIKEACDE 64  
DB 7 IPEKTYGKPLKPHLEKEQLSGSLMRLADELGIPEFDFGVSVSGHNLVAEVCDE 66  
QY 65 SRPEKNLSQALKPVRDAGSLFTSMHEKWKAKHMLLPSEFOQAMKYNHAMVUAV 124  
DB 67 KRFEPKNGKGLQKREFGSDLFVSWHEPWOQKAHMLLPSEFOQAMKNGHSMVDIAT 126  
QY 125 QLVQMERLNADAEIEVEPDMTRLTLDITIGLGFENYFNSFYRQPHFITSMWRALDEA 184  
DB 127 QLVQMERLNADAEIEVEPDMTRLTLDITIGLGFENYFNSFYRQPHFITSMWRALDEA 186  
QY 185 MNKLQANPDDPAYDENKROFOEDIKYANDLVKIIADRKASGQS--DILLTHMLNGKDP 243  
DB 187 MNQSKRLGLQDKMVKTKLQFOKQIEVNSLVDMIAERKANPDENIKDILLTMLVAKDP 246  
QY 244 EFGPEPLDENIRYQITFLNGHTTSGLSFALYFLVKAPHVUQKAAEAAVLUVVP 303  
DB 247 VTGGLTLDENIRYQITFLNGHTTSGLSFALYFLVKAPHVUQKAAEAAVLUVVP 306  
QY 304 SYKQVOKLKYVQWLNELRLMPAPAPFSLYAKEDTVLGGEPLEKDELMVLLPOLHR 363  
DB 307 EYKQIQKRTIRVNLNETLRLYTPAPAFSLYAKEDTVLGGEPLEKDELMVLLPOLHR 366  
QY 364 KTIWGDVEEERPERFENPSAIPQHAKRPFNGORACIGQOFALHEATLVLMMLKHEDF 423  
DB 367 QNANGPDAEDRPERFEDPSIPHHAYKPFNGORACIGQOFALHEATLVLMMLKHEDF 426  
QY 424 EDHNYELDIKETITLKEGVVYAKSKKIPLGIPSESTQS---AKYAKKAKENAHNT 480  
DB 427 INHGYELKIKETITLKEGVVYAKSKKIPLGIPSESTQS---AKYAKKAKENAHNT 484  
QY 481 PLVLYVSGNMGTAEGTADILMSKGFAPQVATLDSHAGNLREGAVLIVTASVNGHP 540  
DB 485 PLVLYVSGNMGTAEGTADILMSKGFAPQVATLDSHAGNLREGAVLIVTASVNGHP 544  
QY 541 PDNAKQFVMDLQASADEVKGVRYSVFQCGDKMAITTYOKVPAFIDETLAKGAENADR 600

DB 545 PDNAKQFVMDLQASADEVKGVRYSVFQCGDKMAITTYOKVPAFIDETLAKGAENADR 604  
QY 601 GEAADSDDEGTYEWEERHEHMSDVAAVFNIDLENSDSTLSLQFVDSAADMLAKMG 660  
DB 605 GEBDADDFESRESSENNFWKETMAFPINELAQEDRPSLITLSATEPVPKAKG 664  
QY 661 AESTNVASKELOQPSARSTRHLEIEPKASVQEGDLGVIPNNYEGIVNRVAFGL 720  
DB 665 AFGIYLERLEQTAASTRSTHIEIEIPAGTYKEGDIIGILPKNSRELVOVRVSRFGL 724  
QY 721 DASQIRLEAEKLANHPLAKTVSEELL--QVVELQDPTVTRQVAMAKTYCPKHYE 779  
DB 725 QSNHVKVGSAAH--MHLPMDRPIKVVLLSSVLEQEPASRLQLELASLYVCPHQYE 783  
QY 780 LEALTEKQA--YEQVLAKEITLMLELEKYPACEMKSEFIALLPSPRYGSISSPRVD 838  
DB 784 LEQVSDDGTYEQVLAKEITLMLELEKYPACEMKSEFIALLPSPRYGSISSPRVD 843  
QY 839 EKQASITVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDEPPL 898  
DB 844 ANIVSWTGVVAKASVSGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDEPPL 903  
QY 899 IMVGEPTGVAPPRGFYQARKOLKEQOSLGEHALYFGCSPHEDYIOEELNAQSEGI 958  
DB 904 IMVGEPTGVAPPRGFYQARKOLKEQOSLGEHALYFGCSPHEDYIOEELNAQSEGI 963  
QY 959 TLHTASRNPNOKTYOVHMEODGKLELLEDOGHAFYICGDSQMAVAVENTLMSYA 1018  
DB 964 TIRCRSRVENEKGVYQHLKODTYKMLTLEKGNHYVCGDSQMAVAVENTLMSYA 1023  
QY 1019 DVHQVEADARLMLQLEBKGRYAKDVWAG 1048  
DB 1024 ABRKASQESASVWLQKLDQDRRYKDVWAG 1053

RESULT 4  
NCPR MOUSE STANDARD; PRT; 677 AA.  
AC P37040;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).  
GN Mus musculus (Mouse).  
OS Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ddv;  
RX MEDLINE=94281246; PubMed=8011664;  
RA Ohtsuka S., Ishizaki K., Kametaki T., Shimikiri N.;  
RT "Mouse NADPH-cytochrome P-450 oxidoreductase: molecular cloning and functional expression in yeast."  
RL Biochim. Biophys. Acta 1186:137-141(1994).  
CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2 ferricytochrome.  
CC -!- COFACTOR: FAD AND FMN.  
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE REDUCTASE.  
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D17571; BAA04496.1; -.
DR HSSP; P00388; IANO.
DR SWISS-2DPAGE; P37040; MOUSE.
DR MGI; MGI:97744; Por.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00175; NAD_binding_1.
DR Pfam; PF00258; Flavodoxin; 1.
DR Pfam; PF00667; FAD binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FMNCR.
DR Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
DR Membrane; Acetylation.
DR MOD RES 0 BY SIMILARITY.
FT INIT MET 0 ACETYLATION (BY SIMILARITY).
FT NP_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 529 547 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 624 640 NADP (ADP PART) (BY SIMILARITY).
SQ SEQUENCE 677 AA; 76912 MW; 0065C14D0E1C5E9F C6C64;

Query Match 14.3%; Score 778.5; DB 1; Length 677;
Best Local Similarity 32.3%; Pred. No. 2.6e-36;
Matches 212; Conservative 106; Mismatches 267; Indels 71; Gaps 22;

QY 444 FVFAKSKKIP-----LGGIPSPTEQS-AKVKRKAENAHNTPLVYVYSGMNGAEGPAR 498
DB 41 FIFKKKEEIEPFSSKIQTTPAPVKESSVEKMKTKGRN-----IIVFGSGTGAEEFAN 95
QY 499 DLADIAMSKGPAQVATLDH-----AGNLPR--EGAVLITVASY-NGHPDNAKQFVWL 551
DB 96 RLSDAHRVYGMKGSADPEEYDLADLSLPEIDKSLVFCVATGEGPPTNADQFVWL 155
QY 552 DQASADEVKYRYVFGCGDKMATYQKVA--FIDETLAAGAENIADRGEDASDD 608
DB 156 QETDVD-LTVYKFAVFGIGNK---TYEHFNAMGYVDQRIEOLGAQRIFELGLDDGN 210
QY 609 FEGTYEERHEHMSDVAAFYNLDIENSEDNKSTSLQVDSAADMPPLAKMH----- 659
DB 211 LEEPFITWKEQFPWAVCFEVEATGESSIRQYELVNH---DMDTKAVITGEGRLKS 267
QY 660 -----GAFSTNVASKELQPGSASRTHLEIEL-PKEASYOEGDHLGVIPRNY 707
DB 268 YENCKRPEDAKNPFLAATTRKLNQ--GTERHMLHLEIDSKIRYSGDHVAVYPRND 326
QY 708 EGIYNRVTAARG--LDASQQRLEAEKLAHLPLAKTVSVEELLQYVELDDPYTRIQLR 765
DB 327 STLVAQGEIIGADLDVMTSLNLDSEENKNGPPECPFTYATATYUADITNP-PRITVL 385
QY 766 AMAKTVCP-----HKVELLEALKEQAYKEOVLAKLIMLELEKYPACEMKPFSERIA 819
DB 386 YELQVAYSEPEQEHLMHMASSGEGKELYLSWVEARRHLTALQDPSPRPPIDLCE 445
QY 820 LLPSPRPVYSSISPRVDEKQASTIVSVSGEAMSGYGEYKGIASNYL-----AEIQE 873
DB 446 LLPRLQAYVSIASSSKVHPNSVHICAVAVEAKSGVNV-KGVALTSLRKEPARGENGR 504
QY 874 GDITTCFISTQSEETLPKDETPYIMVPGTGAFFPGVQARKQLKEGQSGISEAHLY 933
DB 505 RALVPMFVR--KSGFRLPFKPTPIVINGPVGVAFFMGFIQERAMLEEGKEVGETILY 562
QY 934 FGCRSPHEDYLYOELENAQSEGITT-LHTAFSRPNPNPKYVYVHVMQDDKXLIELDDQ 992
DB 563 YGCRSRDEDIYLYREBELAFHKQGAULTQUNAFSR-EOAHKQYVYVHLEKXELHMKLIHE 621

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QY 993 -GAHFYICGDSQMAPAVEATLTKSYADVHQSADARLMLQOLEEKRYAKVMA 1047
DB 622 GAHAIYVCGDARNMAKQVNTFYDIVAEFQPMHTQAVDVYKXLMTGRYSLDWS 677

RESULT 5
NCPR RAT ID NCPR RAT STANDARD; PRT; 677 AA.
AC P00388;
DT 21-JUN-1986 (Rel. 01, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-JUN-2002 (Rel. 41, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).
GN POR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85140278; PubMed=3919392;
RA Porter T.D., Kasper C.B.;
RT "Coding nucleotide sequence of rat NADPH-cytochrome P-450
RL Proc. Natl. Acad. Sci. U.S.A. 82:973-977(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86163762; PubMed=3082610;
RA Murakami H., Yabuaki Y., Ohkawa H.;
RT "Expression of rat NADPH-cytochrome P-450 reductase cDNA in
RL Saccharomyces cerevisiae.";
RN [3]
RP SEQUENCE OF 413-677 FROM N.A.
RX STRAIN=Mistat; TISSUE=Liver;
RL MEDLINE=9104888; PubMed=2125483;
RA Porter T.D., Beck T.W., Kasper C.B.;
RT "NADPH-cytochrome P-450 oxidoreductase gene organization correlates
RL with structural domains of the protein.";
RN [4]
RP Biochemistry 29:9814-9818(1990).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=97385116; PubMed=9237990;
RA Wang M., Roberts D.L., Paschke R., Shea T.M., Masters B.S.S.,
RL Kim J.-J. P.;
RT "Three-dimensional structure of NADPH-cytochrome P450 reductase:
RL prototype for FMN- and FAD-containing enzymes.";
RN [5]
RP Proc. Natl. Acad. Sci. U.S.A. 94:8411-8416(1997).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.80 ANGSTROMS) OF MUTANTS.
RX MEDLINE=21369908; PubMed=11371558;
RA Hubbard P.A., Shen A.L., Paschke R., Kasper C.B., Kim J.-J. P.;
RT "NADPH-cytochrome P450 oxidoreductase. Structural basis for hydride
RL and electron transfer.";
RN [5]
RP J. Biol. Chem. 276:29163-29170(2001).
RX -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
RL TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
RX TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
RN [5]
RP -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
RX ferricytochrome.
RN [5]
RP -1- COFACTOR: FAD AND FMN.
RX -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
RN ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
RX -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
RN FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
RX NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
RN REDUCTASE.
RN [5]
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RX use by non-profit institutions as long as its content is in no way
RN

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DR InterPro; IPR001709; FPN\_cyt\_redctase.  
 DR InterPro; IPR001094; Flavodoxin like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 DR Pfam; PF00175; NAD binding, 1.  
 DR Pfam; PF00258; flavodoxin, 1.  
 DR Pfam; PF00667; FAD binding, 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 KM Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
 Membrane; Acetylation.  
 FT INT MET 0  
 FT MOD\_RES 1 1 ACETYLATION (BY SIMILARITY).  
 FT NP\_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).  
 FT NP\_BIND 528 546 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NP\_BIND 623 639 NADP (ADP PART) (BY SIMILARITY).  
 FT CONFICT 54 54 S -> T (IN REF. 2).  
 FT CONFICT 163 163 T -> S (IN REF. 2).  
 FT CONFICT 174 174 N -> D (IN REF. 3).  
 FT CONFICT 339 339 T -> A (IN REF. 3).  
 FT CONFICT 378 378 N -> D (IN REF. 3).  
 FT CONFICT 400 400 Q -> E (IN REF. 3).  
 FT CONFICT 446 446 R -> L (IN REF. 2).  
 FT CONFICT 502 502 N -> D (IN REF. 3).  
 FT CONFICT 508 508 V -> L (IN REF. 2 AND 3).  
 FT CONFICT 674 674 D -> N (IN REF. 3).  
 SQ SEQUENCE 677 AA; 76701 MW; 26073A0B97EEBDF CXC64;

Query Match 14.1%; Score 769; DB 1; Length 677;  
 Best Local Similarity 31.9%; Pred. No. 8.9e-36;  
 Matches 224; Conservative 109; Mismatches 275; Indels 94; Gaps 27;

QY 401 IGGQFAHEAT-----LVLMMLKHPDEHNTN--ELDIKETLT--LKEGFGVYAKS 450  
 DB 15 VAEVSLEFSATDMLFSLIVGLTYWTFKKKKQVEFFSKITETTSSVKQSSFF----- 69  
 QY 451 KKILGIGIPSPSTEOSAKKVKKAKENAHNTPLVLYGSMGTAGTARDLADIMSKGFA 510  
 DB 70 -----EKMKKTGRN-----IIFYSGQTGTAEFFANRLSKDAHRYGMR 107  
 QY 511 PQVATLD---SHAQNLPR-EGAVLI-VTASY-NGHPEDNAKQFVDWIDQASADEVQVR 563  
 DB 108 GMAADPEEYDLSDSLPEIENALAVFCMATYGEEDPDNADQFDWLGQADVDV-LTGVK 166  
 QY 564 YSVSGCGDKMATYQKVPK---FIDETLAKGAGENTDREGADASDFEGTYEWEPEHM 620  
 DB 167 YAVFGLGNK---TYEHFNAMGKYVDKLEQLGAQRLFDLGLGDDGMLIEDFTWRQF 222  
 QY 621 WSDVAAYFNLDIENSSEDKSTLSIQF--VDSAA-----DMLAKWGAFS 663  
 DB 223 WPNVCEHGVATGESESIROYELVHTDMPTAVVYTGEMRLKSYENOKPPPAKPF 282  
 QY 664 TNVVASKELOOPGSAARSTRHLEIL-PEASVQESDHLGVI-PRNVEGIVNVTARFGIDA 722  
 DB 283 AVVTTNRKLNQ-GTERHLMHLELIDISDKIRYESGDHVAVPANDSALVNLGELIGTDL 341  
 QY 723 SQQI---RLAEBEKLAHLPLAKTVSVBELQYVELQDPVTRTQRLMAAKTVCPRHAVE 779  
 DB 342 DIVASLNLNDESNRHPFPCPTTYRT-ALTYVYDITNPRTNYVELAQVASESESEQ 400  
 QY 780 LEALIE-----KQAVKEQVLAKRLTMLLEKYVPACEKMFSEFALPISIRPVYSSSS 834  
 DB 401 LRKVASSGEGKEKELYLSNVVAKRHIIILIDYPSLRPIHLCEPLRLQARIYSSSS 460  
 QY 835 PRVDEKQASTVSVSGEAMSGYGEYKGIASNYL-AELQEGDT-----ITCFISTPOSEF 888  
 DB 461 SKVHPNSVHICAVVVEYETKSGRVN-KGVATSWLRAKPEAGENGRAVLPVEVR--KSQF 517  
 QY 889 TLRPDPEPLMNGRGTVAPFRGVQARKOLKEGQSLGAHALYFGRSHEDELYQEE 948  
 DB 518 RLFPKATTPVIMVGEGTVAPFIFGIORAWLLOEGKEVGETLLYYGCRSDEDELYREE 577

QY 949 LENAQSEGIIT-LHTAFSRMNPQ-KTYQVWNEQDGKLIIELL-DQGAHYICGDSQM 1005  
 DB 578 LAQFHAKGALTPLRSVAFSR--EQPQKYVQHLHLKRDKEHMLKLIHDGAIHYICGDARNM 635  
 QY 1006 APAYEATLMKSYADVHVSEADARLMICQLEEGRYAKDQWA 1047  
 DB 636 ARDVQNTFCDIVAEGGMEHAQADVVKRLMTKGRVSLDWS 677  
 RESULT 7  
 NCPR\_RABIT STANDARD; PRT; 679 AA.  
 ID NCPR\_RABIT  
 AC P00389;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).  
 GN POR.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=87137361; PubMed=1029050;  
 RA Karagiri M., Murakami H., Yabusaki Y., Sugiyama T., Okamoto M.,  
 RA Yamano T., Okawa H.,  
 RT "Molecular cloning and sequence analysis of full-length cDNA for  
 RT rabbit liver NADPH-cytochrome P-450 reductase mRNA."  
 RL J. Biochem. 100:945-954(1986).  
 RN [2]  
 RP PARTIAL SEQUENCE OF 1-81.  
 RC TISSUE=Liver;  
 RX MEDLINE=82167456; PubMed=602823;  
 RA Black S.D., Coon M.C.,  
 RT "Structural features of liver microsomal NADPH-cytochrome P-450  
 RT reductase. Hydrophobic domain, hydrophilic domain, and connecting  
 RT region."  
 RL J. Biol. Chem. 257:5929-5938(1982).  
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
 CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
 CC ferriocytocrome.  
 CC -1- COFACTOR: FAD AND FMN.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
 CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
 CC REDUCTASE.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; D00101; BA00063.1; -  
 CC EMBL; X04610; CA28279.1; -  
 CC PIR; A25505; A25505.  
 CC PIR; A05233; A05233.  
 CC HSSP; P16435; IBI1C.  
 CC InterPro; IPR003097; FAD binding.  
 CC InterPro; IPR001709; FPN\_cyt\_redctase.  
 CC InterPro; IPR001094; Flavodoxin like.  
 CC InterPro; IPR001226; Flavodoxin.  
 CC InterPro; IPR001433; Oxred\_FAD/NAD(P).  
 CC Pfam; PF00175; NAD\_binding; 1.

DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00667; FAD\_binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FPNCR.  
 KM Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
 KM Membrane; Acetylation;  
 FT MOD\_RES 72 ACETYLATION.  
 FT MOD\_BIND 171 FMN (PYRIDINE PART) (BY SIMILARITY).  
 FT MOD\_BIND 315 FAD (ADP PART) (BY SIMILARITY).  
 FT MOD\_BIND 452 FAD (FLAVIN PART) (BY SIMILARITY).  
 FT MOD\_BIND 530 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT MOD\_BIND 625 NADP (ADP PART) (BY SIMILARITY).  
 FT CONFLICT 40 YW -> NY (IN REF. 2).  
 FT CONFLICT 53 E -> N (IN REF. 2).  
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 Best Local Similarity 31.7%; Pred. No. 8.9e-35; Indels 96; Gaps 24;  
 Matches 212; Conservative 111; Mismatches 250;  
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 DB 42 FLRRKKKEVEPTFKIQAPTSSSVKSESVFKKKTKGRN-----IVFYSGQTAEFA 96  
 QY 498 RDLADLAMSGRFAPQVATLDH---AGNTPREGAVLIV--TASY-NGAPPDNAKQFVDW 550  
 DB 97 NRSLSKDAHRYGMGMADPEEYDLADLSLPEINNALAVFCMATYGGEDPTDADQFVDW 156  
 QY 551 LDQASDEVGVYRVVSGCGDKMATTYQVPA---PIDETLAKAGKENTADGENDASD 607  
 DB 157 LGQTDVVD-LSGVKKAFAVGLNKK---YEFHFNMAKTKVDRLEQLGQRIFFELMGDDA 211  
 QY 608 DPEGTVEEMREHNSDVAAAYFNLDIENSEDNKSTLSIQFVDSADMDPLAMH----- 659  
 DB 212 NLEDEFTWMEQWPAVCEHFGVATGESESSIRQYELV---HTDDIVAVYGGEMRLK 268  
 QY 660 -----GAFSTNVVASKELQOPGASRSTRHLEIL-PKEASVGGDHLCVTPRN 706  
 DB 269 SYENOKPPDPANRPLATVTNTRKLNQ-GTERHLMHLELIDISDKIRYESGDHVAVVPAN 327  
 QY 707 YEGIVRVTRFGLDASQOI---RLEAEERKLAHLPL-----AKVSV 746  
 DB 328 DSAIVNQLGEITLADLDVVSINLNDSESKKHPFPPTSYRTALTYLDTNPPRTNVL 387  
 QY 747 EELLQVVELQDPVTRQLRAMAAKTVPKPKVELEALLEKQAYKEOVLAKRLTWLELLEK 806  
 DB 388 YELAQYA--ADPAQOEQLRKMASSSG-----EGKELVLSNVEARRHLAILQD 434  
 QY 807 YPACEMKFEFFIALPISIRPRVYSSSPVDEKQASITVSVSGEAMSGYGEYKGIASN 866  
 DB 435 YPSLRPPIDHLCPLRLQARYSIASSSKVHPNSVHICAVAVEYETKARLN-KGVATS 493  
 QY 867 YL-AELOEGDT-----ITCFISTPQSEFTLPKQBPETLIVNGVETGYAPRFGVQARKQ 920  
 DB 494 WLAKKRPAGNGRGLVPMFVR--KSGFRLPFKATTVIVNGPOTGAPPIGFOEAWL 551  
 QY 921 KEQGOSLGEAHLFYGCSPHEDYLYOBELENAOSEGIT-IT-LHTAFSMPQPKTYVOHW 979  
 DB 552 RQGGKEVGETLYYCGRAEDYLYREELNGFQKQDGLSOLNVAFSSEQQ-KYIVQHL 610  
 QY 980 EODGSKLIELLD-GAHFYTCGDSQONAPAVEATLMSYADVHGVSEADARLWLOOLEEK 1038  
 DB 611 RRDKEHLMRLIHGGAHYVCGDARNMARVDQNTFYDVALGMEBAQAVDVYKKLMTK 670  
 QY 1039 GRVAKDQWA 1047  
 DB 671 GRVSLDQWS 679

DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).  
 GN POR OR CYPR.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=90105390; PubMed=2513880;  
 RA Hanin M., McManus M.E., Birkett D.J., Lee T.D., Shively J.E.;  
 RT "Structural and functional analysis of NADPH-cytochrome P-450  
 RT reductase from human liver: complete sequence of human enzyme and  
 RT NADPH-binding sites.";  
 RL Biochemistry 28:8639-8645(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92198003; PubMed=1550342;  
 RA Shepard E.A., Palmer C.N., Segall H.J., Phillips I.R.;  
 RT "Quantification of cytochrome P450 reductase gene expression in human  
 RT tissues.";  
 RL Arch. Biochem. Biophys. 294:168-172(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Czerwikski M., Sahni M., Madan A., Parkinson A.;  
 RT "Polymorphism of human CYPOR: expression of new allele.";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Murakami H.O., Ogawa H., Nisimoto Y.;  
 RT "cDNA cloning and characterization of NADPH-cytochrome P-450 reductase  
 RT in human HL-60 cell.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 61-241.  
 RX MEDLINE=99156068; PubMed=10048323;  
 RA Zhao Q., Modi S., Smith G., Paine M., McDonagh P.D., Wolf C.R.,  
 RA Tew D., Lian L.Y., Roberts G.C., Driessen H.P.;  
 RT "Crystal structure of the FMN-binding domain of human cytochrome P450  
 RT reductase at 1.93 A resolution.";  
 RL Protein Sci. 8:298-306(1999).  
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
 CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON  
 CC TRANSFER FOR HEME OXYGENASE AND CYTOCHROME B5.  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferri-cytochrome = NADP(+) + 2  
 CC ferri-cytochrome.  
 CC -1- COFACTOR: FAD AND FMN.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE  
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
 CC FLAVODOXIN. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
 CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
 CC REDUCTASE.  
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 CC  
 CC EMBL; S90469; AAB21814.1; -  
 CC EMBL; AF258341; AAG09798.1; -  
 CC EMBL; AB051763; BAB18572.1; -  
 CC PIR; A33421; A33421  
 CC PDB; 1BIC; 24-NOV-99.  
 CC Genew; HGNC:9208; POR.  
 CC MIM; 124015; -



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DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001709; FPN_cyt_reductase.
DR InterPro: IPR001094; Flavodoxin like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00175; NAD_binding_1.
DR Pfam: PF00258; Flavodoxin; 1.
DR Pfam: PF00667; FAD_binding; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
KM Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
KM Membrane; Acetylation; Polymorphism; 3D-structure.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
FT NP_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 313 324 FAD (ADE PART) (BY SIMILARITY).
FT NP_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 528 546 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 622 638 NADP (ADE PART) (BY SIMILARITY).
FT VARIANT 499 499 A->V.
FT VARIANT 550 550 /FTID=VAR_004617.
FT VARIANT 550 550 R->Q.
FT CONFLICT 404 404 /FTID=VAR_004618.
FT CONFLICT 517 517 M->L (IN REF. 4).
FT CONFLICT 536 537 F->L (IN REF. 2 AND 4).
SQ SEQUENCE 676 AA; 76558 MM; 983EA13797020D70 CRC64;
Query March 14.1%; Score 767; DB 1; Length 676;
Best Local Similarity 32.4%; Pred. No. 1.1e-35;
Matches 211; Conservative 113; Mismatches 264; Indels 64; Gaps 23;
QY 444 FVYAKSKKIP-----LGSIPESTEOS-AKIVRKAENAHNTPLVLVGSNMGTAEGR 498
DQ 41 FLFKKKKEVEPFKIQTLTSSVRESSVEKMKTKGR-----IIVFGSGTGAEEFAN 95
QY 499 DLADIANSKGAPOVATLDSH---AGNLPREGAVLY--TASY-NGHPPNNAQFVDM 551
DQ 96 RLSDARHYGKRGMSADPEEYDLADLSLPEIDNALVFCVATYGEQDPTNADPFYDML 155
QY 552 DQASADEVKGRVSVFGGDNWATTYOKVPA---FIDETLAAGAENIADRGESDSD 608
DQ 156 QETVVD--LSGVKVFVGLGNK---TYEHFAMGKYVDKLEQJGAKRIFELGJGDDGN 210
QY 609 FEETYEEMREHMSDVAAVFNLDIENSSEKSTLSLOP---VDSA---ADMPLAKM-- 659
DQ 211 LEEDFITMREGFPAVCHFEVATGSESSIRQVELVHTDIDAKVYMGMSGLKSYEN 270
QY 660 -----GARSTNVASKELOQPGSARSTHLEIEL-PKASVIOEGDHLGVIPRYEG 710
DQ 271 QKPEFDANKPFLAVTTNRKLNQ--GTERHMLHLEIDISDKIRYESGDHVAVVPANSD 329
QY 711 VNRVTARFG--LDASQOIRLEAEKLAHLPLAKTVSVEELQVVELQVLODPVTRQLRMA 768
DQ 330 VNOGKILGADLDVYMSLNLDESNNKHPPTSTRTALTLYLDITNP-PRTNVLYEL 388
QY 769 AKTVCPPHKVELLEALL-----KQAYKEQVLAIRLTMLELLEKYPACEMKFSFIALP 822
DQ 389 AQVASESEBQELKRMASSGEGKELYLSWVEARHRLIALIQCPSLRPIDHLCLELP 448
QY 823 SIRPRYISISSPRVDEKQASITVSVSGEAMSGYGEYKIASVYL-AELOEGDT---- 876
DQ 449 RLQARYSIASSSKVHPNSVHICAVVVEYETKAGIN-KGVATWMLRAKEPAGENGGRAL 507
QY 877 ITCISITPOSEFTLPKDEPTLIMWGPECTGAPRPGFQAQKLEQOSIGEAHLVRC 936
DQ 508 VPMFVR--KSOFRILPFKATPVLIMWPGTGAAPFGIGFQERAMLRQOQKEVETLLYGC 565
QY 937 RSPHEDLYQEELENAOSEGIT--LHTAFSMNPQPTKYVOHVMEOODSKLIELLDQAH 995
DQ 566 RRSDEYVIREELAQFHHDGALTQLVNAFSEQSH-KYVGHLLKQDREHMLKILEGGAH 624
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DQ 625 IYVCGDARNARVDQNTFYDVALGEMHAQAVDYTKMLTKGRYSLDWS 676
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ID NCPR_CAVPO
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).
GN POR.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley;
RA MEDLINE=93041995; PubMed=1420354;
RA Ongiya S., Goda T., Ishizaki K., Kamataki T., Shiraiki N.;
RT "Molecular cloning and sequence analysis of guinea-pig NADPH-
RT cytochrome P-450 oxidoreductase.";
RL Biochim. Biophys. Acta 1171:103-105(1992).
[2]
RP ERRATUM.
RX MEDLINE=93385164; PubMed=8373812;
RA Ongiya S., Goda T., Ishizaki K., Kamataki T., Shiraiki N.;
RL Biochim. Biophys. Acta 1174:313-313(1993)
CC -1 FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
CC TO CYTOCHROME P450 IN MICROSOSES. IT CAN ALSO PROVIDE ELECTRON
CC -1 CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferricytochrome.
CC -1 COPACITOR: FAD AND FMN.
CC -1 SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
CC -1 SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
CC REDUCTASE.
CC -1 CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO ORIGINATE FROM MOUSE.
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DQ EMBL: D10498; BAA01385.1; -.
DQ PUR: S27158; S27158.
DQ HSSP: P00388; JAMO.
DQ InterPro: IPR003097; FAD_binding.
DQ InterPro: IPR001709; FPN_cyt_reductase.
DQ InterPro: IPR001094; Flavodoxin like.
DQ InterPro: IPR001226; Flavodoxin.
DQ InterPro: IPR001433; Oxred_FAD/NAD(P).
DQ Pfam: PF00175; NAD_binding_1.
DQ Pfam: PF00258; Flavodoxin; 1.
DQ Pfam: PF00667; FAD_binding; 1.
DQ PRINTS: PR00369; FLAVODOXIN.
DQ PRINTS: PR00371; FPNCR.
KM Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
KM Membrane; Acetylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT NP_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 313 324 FAD (ADE PART) (BY SIMILARITY).
FT NP_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 529 547 NADP (RIBOSE PART) (BY SIMILARITY).

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Qy      925 QSLGEANLHVGCRSPHEDYLYOELENAQSEGITTLTAFSRMNPQTYQVHMEODGK 984
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Qy      985 KLIELL-DQGNHRTICGDSGMAFAVEVLTLMKSVADYHVSADARLMLQOLEKGRYAK 1043
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Db      668 DVMS 671

RESULT 11
NCPR DROME STANDARD; PRT; 679 AA.
ID NCPR DROME
AC 027597; 09VME2;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).
GN CYP OR CG11567.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
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RC STRAIN=Canlon-S; TISSUE=Antenna;
RX MEDLINE=97311413; PubMed=9168130;
RA Hovemann B.T., Sehlmeyer F., Malz J.;
RT "Drosophila melanogaster NADPH-cytochrome P450 oxidoreductase:
RT pronounced expression in antennae may be related to odorant
RT clearance."
RL Gene 189:213-219(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiker S.E., Li P.W., Hoekins R.A., Galle R.F.,
RA Amandides P.G., Scherer S.E., Li P.W., Hoekins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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RA Ballew R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshak S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J., Houck J.,
RA Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jajani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kratz C., Kravitz S., Kulp D., Lai X.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

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RA Liu X., Matvei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostreli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Sanders R.D.C., Scheeler F., Shen H.,
RA Reimert K., Remington K., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Turner R., Venter E., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5. MAY FUNCTION TO
CC CLEAR THE OLFACTORY ORGAN (ANTENNAE) FROM ACCUMULATING CHEMICALS.
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferricytochrome.
CC -1- COFACTOR: FAD AND FMN.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGH IN ANTENNAE.
CC -1- DEVELOPMENTAL STAGE: EMBRYOS AND ADULTS.
CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
CC REDUCTASE.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; X93090; CA63639.1; -
DR EMBL; AE003613; AAF52367.1; -
DR HSSP; P16435; 1B1C.
DR FLYBASE; FBgn0015623; Cpr.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001709; FPN_Cyt_reductase.
DR InterPro; IPR001094; FlavoDOXin like.
DR InterPro; IPR001226; FlavoDOXin.
DR InterPro; IPR001435; Oxred_FAD/NAD(P).
DR Pfam; PF00175; NAD_binding_1.
DR Pfam; PF00258; FlavoDOXin; 1.
DR Pfam; PF00667; FAD binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR Oxidoreductase; FlavoProtein; FMN; FAD; NADP; Endoplasmic reticulum;
KW Membrane.
FT NP_BIND 176 207 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 320 331 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 457 467 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 537 555 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 632 648 NADP (ADP PART) (BY SIMILARITY).
FT CONFLICT 38 39 AA -> VT (IN REF. 1).
FT CONFLICT 45 45 S -> T (IN REF. 1).
FT CONFLICT 132 132 I -> T (IN REF. 1).
SQ SEQUENCE 679 AA; 76346 MW; C6387C111A0DB8A CRC64;
Query Match 13.3%; Score 725.5; DB 1; Length 679;
Best Local Similarity 29.8%; Pred. No. 2.4e-33;
Matches 191; Conservative 113; Mismatches 257; Indels 79; Gaps 21;
Qy 460 SPSTEGSAKYRKAENAHNTPLVLYGSMNGTAGRABDLADAMS---KGFA--POVA 514
Db 67 SASDNSFTKLUK-----ASGRSLVVFYGSQGTGEERGLAKGIRYRLKGMVADPEEC 121

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OY 5145 TLDS--HAGNI-PREGAVI I V T V A S Y N G H P D N A K Q V D M L D Q A S A D E V G V R V S Y V G C B K 5172
Db 122 DMEBLLOJLKD I N S I A V F C I A T Y G G C D P P D N M E Y E W I T S D G V - L S C L N A Y V A V G L G K 180
OY 5173 N W A T T Y O K V P A F I D E T L L A K A G A N E I A D R G E A D A S D F E G T Y E M E R E H M S D V A A F E N D I 632
Db 181 T Y - B H Y N N V A I Y V D K R L E B E L G A N N R F E L G D D D A N I E D D F I T W D R F P A C H F G -- I 237
OY 633 E N S E D N K S T L S I Q F V D S A A D M P ----- L A C H ----- G A F S T I N V A S K E I Q 673
Db 238 E G G G E A V I R O Y R L E O P D V O P D R I Y T G E I A I A H S I O N O R P P F D A K N F L A P I K N R E I H 297
OY 674 O P G A S A R S T R H I E I L P - K E A S Y Q E B D I G V I P R N E G Y N R T A R F G L A S --- Q O I N L E 729
Db 298 K - G G G R S C M H I B L S I E G S K M R Y D A G D H V A M F V P N K S I V E K R G O U C N A D L D T V F S L I N T D 356
OY 730 A E E K T A H I P ----- L A K T V S V E L L Q V Y E L O P D V T R T O L R A A A K T V 772
Db 357 T D S S K H H P P C T T Y R T A L T H Y L E I T A I P R H I L K E L A E Y - C T B E K E L L R S M A -- S I 412
OY 773 C P H K V E L E A L L E K O A Y K E Q V L A K R L T M L E L I E K Y P A C E M K S E F T A L P S I R P Y I S I S 832
Db 413 S P E ----- G K E K Y S W I O D A C R N I V H I L E D I K S C P P I D H C E L L P R L O P R Y I S I S 463
OY 833 S S P R V D E K O A S I T V S V G E A M S G I G E Y K G I A S N T A I E I Q --- E G D I T C I S T P O S E F 888
Db 464 S S A K I H P D V H T A V L A V E Y K T P T G I N - K G A V T T L K R K O P G S E E V K V P E I R -- K O F 520
OY 889 T L P K O P E T P L I M V G G C T G V A P R G V O A R K O L E G O S I G E A H L T F G C S P H E D I T Y O E 948
Db 521 R L P T K E P E I P I M V G C T G L A P R G I O E R O P L A D B G C K T Y G S E I L P G C R K S E D I T Y E B E 580
OY 949 L E N A O S E G I T L T H A F S S R M P N O P K T Y V O H V E O D E K U L I E L L D O G - A H F Y I G D S O M A P 1007
Db 581 L E E W Y K K T L N L K A F S R D O G K - K Y V O G H L E O D A D L I M N V I G E N K G H Y I C G D A C M A V 639
OY 1008 A V E A T L M S Y A D V H O V S E A D A R L M L O Q L E K R Y A K D W A 1047
Db 640 D V R N I L V I K I L S T G K M S E A D A V O Y I K R M E A O Q R Y A D W S 679

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RESULT 12	ID	NCPR_SALT	STANDARD;	PRT;	601 AA.
AC	PI9618;				
DT	01-FEB-1991	(Rel. 17, Created)			
DT	01-FEB-1991	(Rel. 17, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR)				
DE	(Fragments).				
OS	Salmo trutta (Brown trout).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;				
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.				
OX	NCBI_TaxID=8032;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=88008061; Pubmed=3116019;				
RA	Urenjak J., Linder D., Lumper L.;				
RT	"Structural comparison between the trout and mammalian hydrophilic				
RL	domain of NADPH-cytochrome P-450 reductase.";				
RL	J. Chromatogr. A 397:123-136(1987)				
CC	-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP				
CC	TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON				
CC	TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.				
CC	-1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2				
CC	ferricytochrome.				
CC	-1- COFACTOR: FAD AND FMN.				
CC	-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE				
CC	ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.				
CC	-1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL				
CC	FLAVOXYDINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN				

CC	NADP; REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE REDUCTASE.
CC	
DR	PIR; A28577; A28577.
DR	HSSP; P16435; IBLI.
DR	InterPro; IPR001709; RPN_cyt_redtase.
DR	InterPro; IPR001094; Flavodoxin_like.
DR	PRINTS; PR00369; FLAVODOXIN.
DR	PRINTS; PR00371; PNCR.
KW	Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum; Membrane.
KW	
FT	NON_TER 1 1
FT	NON_CONS 426 427 .
FT	NON_CONS 434 435 .
SQ	SEQUENCE 601 AA; 68304 MW; BC801767DELD4C9 CRC64;

Query Match	13.2%;	Score 723;	DB 1;	Length 601;
Best Local Similarity	30.2%;	Pred. No. 2.8e-33;		
Matches 195;	Conservative 106;	Mismatches 239;	Indels 106;	Gaps 21;

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Qy 459 P$P$TEGSA--KYVRKKAENAHNTPLVLVIGSNMGT$EGTRADLADJAMS$KGAPOYATL 516
Db 5 PABTQ$T$FLEKAKKTKGRN-----IYFPG$Q$GT$EEEPNRJ$SKOAHK$GMSMAADP 59
Qy 517 D-----SHAGNL$PREGAVLIY--TASY--NGHPPD$NAKQFVDMLDQASAD$EVNGVRY$VFGC 569
Db 60 E$YDMS$EL$RLAEIGNSLAI$FCMATYGE$DPTD$AO$FYDML--Q$TDGQ$IG$S$VNVY$P$VAL 118
Qy 570 GDKM$WATTYQ$KVP$FIDETL$AAKGAENIADRG$EAD$DDE$BGT$YEENR$EHMS$V$AA$YFN 629
Db 119 GDKTY--E$HYNMGAYVDK$RL$EELGAKKVP$FLGMDGDD$DGNLEED$FVTR$EOP$FPM$CERFG 177
Qy 630 LDIENSEDNK$TSL$Q$FV$D$A$ADP$PLAKM$-----GA$F$TN$V$AS 669
Db 178 V$ASG$E$D$S$V$RQ$YELK---E$HND$NM$K$VY$T$G$EL$RLK$S$ETQ$K$P$PD$AK$P$FLA$P$TVN 234
Qy 670 K$ELOQ$P$S$AS$TR$HLEI$P--K$EAS$YOE$D$H$G$VY$P$N$Y$E$G$V$NR$V$TAR$F$GLD$S$Q$O$IRL 728
Db 235 R$K$N$K$G$E$L$H$K--M$H$E$V$D$IT$G$SK$IR$Y$E$G$D$H$V$AY$P$TN$N$Y$V$IR$L$Q$O$IG$V$D$S$V$ISL 293
Qy 729 EAB$E$K-----L$H$L$P$L$A$K$T$V$S$E$E$IL$Q$Y--V$E$L$O$D$P$TR$Q$RLR 765
Db 294 N$N$D$E$E$N$K$K$H$P$P$C$P$T$Y$T$A$L$H$Y$D$I$H$P--R$TN$V$L$Y$E$L$O$V$AT$D$L$D$Q$E$N$T$S$MA 351
Qy 766 A$M$A$K$T$C$P$H$K$V$E$L$E$A$L$E$K$O$A$Y$K$E$O$V$A$K$R$L$M$E$L$E$K$Y$P$A$C$E$K$K$F$E$F$IAL$P$SIR 825
Db 352 S$S$A$P$E-----G$K$AL$Y$Q$S$V$L$E$D$N$R$I$A$L$I$E$D$L$E$P$L$R$P$D$H$L$C$E$L$M$R$LO 397
Qy 826 P$R$Y$I$S$S$P$R$V$D$E$K$O$A$S$T$V$S$V$V$G$E$A$M$S$G$Y$EY--K$G$I$A$N$Y$L$A$E$L$Q$E$D$T$T$C$F$IST 883
Db 398 A$R$Y$S$I$A$S$S$K$V$H$N$S$I$H$I$C$A$V$L-----E$Y$K$T$G$V$A$T$M$L$K$YR----- 437
Qy 884 P$O$E$F$T$L$P$K$D$E$P$P$L$I$W$G$T$G$V$A$P$R$G$F$O$A$K$O$L$E$G$O$S$I$G$E$A$H$L$Y$G$R$S$P$H$E$D$Y 943
Db 438 -K$G$O$F$L$P$F$A$S$N$D$V$I$W$G$E$T$G$I$A$P$M$G$F$I$O$E$K$M$L$E$S$E$K$E$G$E$T$V$L$Y$G$C$H$K$E$D$Y 496
Qy 944 L$Y$O$E$L$E$N$A$O$E$G$I$T--L$H$T$A$F$S$R$M$P$Q$K$T$Y$O$V$H$W$E$O$D$E$K$U--I$E$L$D$G$A$F$I$Y$IGD 1001
Db 497 L$Y$O$E$L$E$Q$A$H$K$K$G$A$L$T$K$I$N$A$F$S$R$E$Q$O--K$Y$V$O$H$L$R$K$K$Q$V$D$M$R$Q$I$H$E$D$Y$A$H$I$Y$IGD 555
Qy 1002 G$S$O$M$A$P$V$E$A$T$I$M$K$S$Y$A$D$V$H$O$V$S$A$D$A$R$L$M$O$L$E$E$G$R$A$K$U$Y$A 1047
Db 556 A$R$N$A$R$D$V$O$T$A$F$Y$E$I$A$E$L$G$M$T$R$O$A$T$D$Y$I$K$L$M$T$G$R$S$O$D$W$S 601

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RESULT 13			
NCPR	PHAAU		
ID	NCPR PHAAU	STANDARD;	PRT; 690 AA.
AC	P3716;		
DT	01-OCT-1994	(Rel. 30. Created)	
DT	01-OCT-1994	(Rel. 30. Last sequence update)	
DT	16-OCT-2001	(Rel. 40. Last annotation update)	
DE	NADP+-cytochrome P450 reductase (EC 1.6.2.4)	(CPR)	(P45OR)
DS	Phaseolus aureus (Mung bean) (Vigna radiata)		

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC Eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
 CC NCBI\_TaxId=3916;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=cv. Beiken; TISSUE=seedling;  
 RX MEDLINE=93219390; PubMed=8464904;  
 RA Shet M.S., Sathasivan K., Arlotto M.A., Mehdy M.C., Estabrook R.W.,  
 RT "Purification, characterization, and cDNA cloning of an NADPH-  
 RT cytochrome P450 reductase from mung bean."  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2890-2894(1993).  
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
 CC TO CYTOCHROME P450.  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
 CC ferriocytocrome.  
 CC -1- COFACTOR: FAD AND FMN.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
 CC -1- PFM: GLYCOSYLATED.  
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN  
 CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
 CC REDUCTASE.  
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 CC -----  
 DR EMBL: L07843; AAA34240.1; -.  
 DR HSSP: P00388; 1AM0.  
 DR InterPro: IPR003097; FAD binding.  
 DR InterPro: IPR001709; FPN\_cyt\_reductase.  
 DR InterPro: IPR001094; Flavodoxin-like.  
 DR InterPro: IPR001226; Flavodoxin.  
 DR InterPro: IPR001433; Oxid. FAD/NAD(P).  
 DR Pfam: PF00175; NAD binding\_1.  
 DR Pfam: PF00258; flavodoxin\_1.  
 DR Pfam: PF00667; FAD binding\_1.  
 DR PRINTS: PR00369; FLAVODOXIN.  
 DR PRINTS: PR00371; FPNCR.  
 KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
 KW Membrane; Glycoprotein.  
 FT NP\_BIND 179 210 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 325 336 FAD (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 465 475 FAD (FLAVIN PART) (BY SIMILARITY).  
 FT NP\_BIND 544 562 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NP\_BIND 639 654 NADP (ADP PART) (BY SIMILARITY).  
 FT CARBOHYD 275 275 N-LINKED (GLUCNA. . .) (POTENTIAL).  
 FT CARBOHYD 339 339 N-LINKED (GLUCNA. . .) (POTENTIAL).  
 SQ SEQUENCE 690 AA; 76506 MW; 592966167E8561DE C6C64;  
 Query Match 13.2%; Score 721; DB 1; Length 690;  
 Best Local Similarity 30.6%; Pred. No. 4,4e-33;  
 Matches 191; Conservative 109; Mismatches 259; Indels 66; Gaps 19;  
 QY 477 AHNTPLLVYSGNNGTAGTARLAD--IAMSKEFAPVATLDSHAGN-----LPRRG 527  
 DB 77 AGKTKVITFGTGTAGFAKALAEIKARYEKAIVVLDVYAADDDVEEKLKES 136  
 QY 528 AVLVTASY-NGHPRDANKQVMDLQASABE---VKVRSVRECGSKMATTYQKPA 583  
 DB 137 LVFPMLATVYGGEPIDNARYFKWTEKDRGVLQKLTGTGVFLGNROY-EHNNKIGK 195  
 QY 584 FIDETLAKGANLADGEADASDPESTYEERHMSDVAAYNLIDENSEDKSTLS 643  
 DB 196 VDEELAEQAKRLVAVAGLGGDDSDIEDFSAMKESLSELD-----QLADEDDANTVS 250  
 QY 644 LQFVDSADM-----PLA-----KMGAFSTNVVASKELQPGSARS 680

DB 251 TPTAALAEVVIHPTASTYDNDNSTANGTEPDIIHPCVAVAVQELKHPESDRS 310  
 QY 681 TRHLEILP-KEASYOEGDLGVI PRNYEGIVARVAFGLDASQOIRLEAEKLAHL- 738  
 DB 311 CHLEPDIQSTSTITDTGHDGVYAENCNTEVETKLGQNDLDFSLHTDQDSTLSG 370  
 QY 739 -----PLAKTVSE-ELQVYELQDPVTRTQLRMAAKTVCPPHKVELEALL- 789  
 DB 371 GSLPPEPGCSRTALARYADLLNPPRKALLALATH-ASEPSDEKELKSSPOGDEX 429  
 QY 790 KEQVLAKRLMLLEKVPACENKFESEFI-ALLPSIRPRYSISSSPRVDEXASITVS 848  
 DB 430 SKWVVSQSRSLVEMAEFPSPAKPPLGVFAIAPRIQPRYSISSSPRPQVHYTCAL 489  
 QY 849 VSGEAMSGVEYGIASNYL-----AELOEGDTTCFISTPOSEFTLPDPETPLIMG 902  
 DB 490 VYGPTEPG-RIHNGVCESTMKNMIPSEKSDCSAPFIR--PSNPLPVDHSPIIMVG 546  
 QY 903 PGTGAPFRGFVQARKQKEQSGSLGEMALVFCGRSPHEDVLYOELENAQSEGIIT-LH 961  
 DB 547 PGTGLAPFRGFLQERVALKEDGVQLGPALEFPCGRNQMPFIVEDELKSFVEQSGISELI 606  
 QY 962 TAFSRMNOQKTYVQVHMEQDGKLLIELDQGAHFIYICGDSQGMARVAFETLKSVDVH 1021  
 DB 607 VAFSR-EGAEKEYVQHKMDKAHLWSLSQGYLYVCGDQAKMARDVHRTLSIVQEOE 665  
 QY 1022 QVSEADARLWLOOLEEKGRYAKDV 1046  
 DB 666 NVDSKRAEALVYKLDQGRRLRDVW 690

RESULT 14  
 NCPR CATRO STANDARD; PRT; 714 AA.  
 AC 005001;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).  
 GN CPR.  
 OS Catharanthus roseus (Rosa periwinkle) (Madagascar periwinkle).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Asterales; eusteoids I; Gentianales; Apocynaceae; Rauvolfioideae;  
 CC Vincet; Catharanthus.  
 CC NCBI\_TaxId=4058;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94035173; PubMed=8220474;  
 RA Meljer A.H., Lopes Cardoso M.I., Voskuilen J.T., de Waal A.,  
 RA Verpoorte R., Hoge J.H.C.;  
 RT "Isolation and characterization of a cDNA clone from Catharanthus  
 RT roseus encoding NADPH-cytochrome P-450 reductase, an enzyme essential  
 RT for reactions catalysed by cytochrome P-450 mono-oxygenases in  
 RT plants."  
 RL Plant J. 4:47-60(1993).  
 RN [2]  
 RP SEQUENCE OF 1-11 FROM N.A.  
 RC STRAIN=cv. Morning mist;  
 RA Lopes Cardoso M.T., Meljer A.H., Rueb S., Queiroz Machado J.,  
 RA Memelink J., Hoge J.H.C.;  
 RA Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP  
 CC TO CYTOCHROME P450 IN MICROSOSES. IT CAN ALSO PROVIDE ELECTRON  
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.  
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2  
 CC ferriocytocrome.  
 CC -1- COFACTOR: FAD AND FMN.  
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE  
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.  
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL  
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN

CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE  
 CC REDUCTASE.  
 CC -----  
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 CC -----  
 DR EMBL: X69791; CAA49446.1; -;  
 DR EMBL: Y09417; CAA70571.1; -;  
 DR PIR: S31502; S31502.  
 DR HSSP: P00388; JAMO.  
 DR InterPro: IPR003097; PAD binding.  
 DR InterPro: IPR001709; FPN\_Cyt\_redctse.  
 DR InterPro: IPR001094; Flavodoxin\_like.  
 DR InterPro: IPR001226; Flavodoxin.  
 DR InterPro: IPR001433; Oxid\_FAD/NAD(P).  
 DR Pfam: PF00175; NAD\_binding\_1.  
 DR Pfam: PF00258; Flavodoxin; 1.  
 DR Pfam: PF00667; PAD binding; 1.  
 DR PRINTS: PR00369; FLAVODOXIN.  
 DR PRINTS: PR00371; FPNCR.  
 DR Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;  
 KW Membrane.  
 FT NP\_BIND 200 231 FMN (PYRIMIDINE PART) (BY SIMILARITY).  
 FT NP\_BIND 348 359 FAD (ADP PART) (BY SIMILARITY).  
 FT NP\_BIND 489 499 FAD (FLAVIN PART) (BY SIMILARITY).  
 FT NP\_BIND 567 585 NADP (RIBOSE PART) (BY SIMILARITY).  
 FT NP\_BIND 661 677 NADP (ADP PART) (BY SIMILARITY).  
 SQ SEQUENCE 714 AA; 78958 MW; DBDD9AF41374CF91 CRC64;  
 Query Match 12.9%; Score 702; DB 1; Length 714;  
 Best Local Similarity 28.8%; Pred. No. 5,4e-35;  
 Matches 189; Conservative 118; Mismatches 274; Indels 76; Gaps 18;  
 QY 445 VVAKSKKIPILGIPSPTEQSAKVKKAKENAHNTPLVLYGSSNGTAGCTARDLADIA 504  
 DB 79 VVEPPKLIIVKSVVEPEIDEGKK-----FTTFGTGTATGAPKALAEBA 126  
 QY 505 MSK--GPAQVATLDSHAGN-----LPREGAVLIVTASY-NGHPDNKQFVMDLQA 554  
 DB 127 KATYKAVIKVIDIDVAADEEYKFRKETLAFILATYDGEPTDNARFYKMFVEG 186  
 QY 555 S--ADEKGVKRVSEFGGDKGMATYKQVAFIDETLAAGAENIADRGADSDDEGT 612  
 DB 187 NDRGDMVKMLQYGVFGIGNRQY-EHFNKIAKVDEKVAEGGKRIYPLVLGDDOCIEDD 245  
 QY 613 YEEHREHMGSDVAAYFNLDIENSEDNKSTLQFV-----DSAADMLAKKHGAF 662  
 DB 246 FAAMRENWVE-----LDNLDEDDTIVSTYTAALPEYRVVFPKXSLISEANGHA 299  
 QY 663 S-----TNVASKELQPGASASTRLIELEPKEA-SYOEGLHVIPIR 705  
 DB 300 NGYANGTVYDAQHPCRSNVAVRKELTPASDRSCTHLDPIAGTSGYGGHVGYYCD 359  
 QY 706 NYGGINRVYARFGDASQOIRLEAEKEKLAH-----PLAKTVSVEELLQYVELQDP 758  
 DB 360 NISGEVEAEARLNLBPETVPSLHADKEDTPLAGSSLPFPFPCCTLRALTLYADLNT 419  
 QY 759 VTRTQIRAMAATVCPPHKVELLEALLE---KQAYKEOVLAKRITMLLEKYVACEKFS 815  
 DB 420 PKRSALLALAAVYSDPEADRLKTLASPAKDEYAGSLVANQSSLEFVMAEPFSAKPLG 479  
 QY 816 EFT-ALLPSIRPVYSSISSPRVDEKQASITVSVSEAMSGYGEYKGIASNYLAE---L 871  
 DB 480 VFPAALAPRLQPRFYSSISSPRMAPSRIVHTCALVY-EKTPGGRIHKGVCSTMMKNAIPL 538  
 QY 872 QEG-DITTCISTISPOSFTLPKDPETPLINVGCTGVAPRGVQAKOLKEGOSIGEA 930  
 DB 539 EESRDGSMWADI FVQSNFKLPADPKVYVIMIGPOTGLAPRGFLQERLALKEGAEIGTA 598

QY 931 HLYFGCRSPHEDLYOEBLEENAGSEGIT-LHTAFSRMPNPQRYVQHWEDGKKLIEL 989  
 DB 599 VFPPGCRNRMKMDIYDELDNHFLEIGALSELVAFSR-EGPTQYVQHKMAEKASDIWM 657  
 QY 990 LDGGAFFYICGDSQMAAPAVEATLMKSYADYHOVSADARLMIQLEEKRYAKDW 1046  
 DB 658 ISDGAYVYCGDKAGMARVHRTLHTIAOEGSMDSIOEGFVKYKQMTGRYLRDVW 714  
 RESULT 15  
 ID NOS2\_RAT STANDARD; PRT; 1147 AA.  
 AC Q06518; P97774; Q35765; Q35766; Q64558; Q64005; Q63267;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)  
 GN (Inducible NOS) (INOS).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Vascular smooth muscle;  
 RX MEDLINE=93191721; PubMed=7680561;  
 RA Nunokawa Y., Ishida N., Tanaka S.,  
 RT "Cloning of inducible nitric oxide synthase in rat vascular smooth  
 RT muscle cells."  
 RL Biochem. Biophys. Res. Commun. 191:89-94(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mistari; TISSUE=Pancreatic islets;  
 RX MEDLINE=95309542; PubMed=7540573;  
 RA Karlén A.B., Andersen H.U., Vissing H., Larsen P.M., Fey S.J.,  
 RA Chatterjee B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,  
 RA Mandrup-Poulsen T., Boel E., Nerup J.,  
 RT "Cloning and expression of cytokine-inducible nitric oxide synthase  
 RT cDNA from rat islets of Langerhans."  
 RL Diabetes 44:753-758(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Astrocytes;  
 RX MEDLINE=9421594; PubMed=7513765;  
 RA Galea E., Reis D.U., Feinstein D.L.,  
 RT "Cloning and expression of inducible nitric oxide synthase from rat  
 RT astrocytes."  
 RL J. Neurosci. Res. 37:406-414(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94039059; PubMed=7693462;  
 RA Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K.,  
 RA Kawasaki H., Sugimura T., Saumi H.,  
 RT "Molecular cloning of a cDNA encoding an inducible  
 RT calmodulin-dependent nitric-oxide synthase from rat liver and its  
 RT expression in COS 1 cells."  
 RL Eur. J. Biochem. 217:37-43(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Hepatocytes;  
 RX MEDLINE=93221515; PubMed=7682072;  
 RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.,  
 RA "Hepatocytes and macrophages express an identical cytokine inducible  
 RT nitric oxide synthase gene."  
 RL Biochem. Biophys. Res. Commun. 191:767-774(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Aorta;  
 RX MEDLINE=94325351; PubMed=7519448;  
 RA Geng Y.J., Almqvist M., Hansson G.K.,

CC "cDNA cloning and expression of inducible nitric oxide synthase from  
RT rat vascular smooth muscle cells.";  
RL Blochum. Biophys. Acta 1218:421-424 (1994).  
RN [7]  
RN SEQUENCE FROM N.A.  
RP Koeuga K., Yui Y., Hattori R., Sase K., Elizawa H., Aoyama T.,  
RA Inoue R., Saayama S.;  
RX "Cloning of an inducible nitric oxide synthase from rat  
RT polymorphonuclear neutrophils.";  
RL Endothelium 2:217-221 (1994).  
RN [8]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=97070590; PubMed=8913516;  
RX Teutsamiehl Y., Kawai Y., Takahara H., Onda T., Miyoshi J.,  
RA Futaki S., Nawa M.;  
RT "Sequence analysis of inducible nitric oxide synthase in rat kidney,  
RT lung, and uterus.";  
RL Biol. Pharm. Bull. 19:1374-1376 (1996).  
RN [9]  
RN SEQUENCE OF 426-788 FROM N.A.  
RP STRAIN=Dahl/Rapp salt sensitive strain; TISSUE=Vascular smooth muscle;  
RX MEDLINE=98195092; PubMed=9535415;  
RA Chen P.Y., Gladish R.D., Sanders P.W.;  
RT "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp  
RT salt-sensitive rats.";  
RL Hypertension 31:918-924 (1998).  
RN [10]  
RN SEQUENCE OF 509-740 FROM N.A.  
RP STRAIN=Wistar; TISSUE=Renal glomerulus;  
RX Saura M., Zaragosa C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;  
RT "Advances in the studies of NO synthase regulation in mesangial  
RT cells.";  
RL Nefrologia 16:35-39 (1996).  
RN [11]  
RN SEQUENCE OF 479-655 FROM N.A.  
RP STRAIN=Sprague-Dawley; TISSUE=Renal glomerulus;  
RX MEDLINE=94276509; PubMed=7516453;  
RA Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,  
RA Klahr S.;  
RT "Location of an inducible nitric oxide synthase mRNA in the normal  
RT kidney.";  
RL Kidney Int. 45:998-1005 (1994).  
RN [12]  
RN SEQUENCE OF 420-479 FROM N.A.  
RP TISSUE=Myocardium;  
RA Michael T., Balligand J.-L.;  
RT "Isolation and characterization of iNOS from rat cardiocytes.";  
RL Submitted (SEP-1994) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE  
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.  
CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +  
CC nitric oxide + N NADP(+).  
CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
CC TETRAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
CC THE ENZYME.  
CC -1- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN  
CC INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE  
CC EXERTED AT THE LEVEL OF TRANSCRIPTIONAL/POSTTRANSCRIPTIONAL  
CC MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY  
CC SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY IN THE  
CC MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE  
CC MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.  
CC -1- INDUCTION: BY INTERFERON GAMMA AND LIPOLYSACCHARIDE (LPS).  
CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC -- send an email to license@isb-sib.ch).
-- -----
DR EMBL; D14051; BAA03138.1; -.
DR EMBL; U26686; AAA85861.1; -.
DR DR EMBL; U03699; AAC13747.1; -.
DR DR EMBL; D12520; BAA02090.1; -.
DR DR EMBL; L12562; ABA41720.1; -.
DR DR EMBL; X76881; CAA54208.1; -.
DR DR EMBL; D44591; BAA07994.1; -.
DR DR EMBL; D83661; BAA12035.1; -.
DR DR EMBL; AF006619; AAC16401.1; -.
DR DR EMBL; AF006620; AAC16402.1; -.
DR DR EMBL; U48829; AAB18620.1; -.
DR DR EMBL; S71597; AAB31028.2; -.
DR DR EMBL; J36063; AAC02242.1; -.
DR PIR; JC1472; JC1472.
DR HSSP; P29477; INOS.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001709; FPN_Cyt_redctse.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(p).
DR Pfam; PF00175; NAD_binding_1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00667; FAD_binding_1.
DR Pfam; PF02898; NO_synthase; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PROSITE; PS60001; NOS; 1.
KW Oxioreductases; NADP; PAD; FMN; Calmodulin-binding;HEME;
KZ Zinc; Metal-binding; Multigene family.
FT BINDING 197..197 HEME (BY SIMILARITY).
FT DOMAIN 506..526 CALMODULIN-BINDING (POTENTIAL).
FT NP_BIND 620..651 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 764..775 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 900..910 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 975..993 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 1073..1088 NADP (ADP PART) (BY SIMILARITY).
FT METAL 107..107 ZINC (BY SIMILARITY).
FT METAL 112..112 ZINC (BY SIMILARITY).
FT CONFLICT 10..10 R -> K (IN REF. 7) .
FT CONFLICT 72..72 H -> Y (IN REF. 1) .
FT CONFLICT 107..107 C -> R (IN REF. 3) .
FT CONFLICT 128..128 D -> V (IN REF. 8) .
FT CONFLICT 130..130 P -> H (IN REF. 3) .
FT CONFLICT 171..171 E -> G (IN REF. 8) .
FT CONFLICT 195..195 P -> S (IN REF. 8) .
FT CONFLICT 248..248 S -> T (IN REF. 3 AND 5) .
FT CONFLICT 264..264 Y -> I (IN REF. 3) .
FT CONFLICT 277..277 D -> E (IN REF. 3) .
FT CONFLICT 348..348 A -> P (IN REF. 1) .
FT CONFLICT 349..349 V -> A (IN REF. 6) .
FT CONFLICT 380..380 F -> L (IN REF. 2 , 7 AND 8) .
FT CONFLICT 395..395 R -> S (IN REF. 4) .
FT CONFLICT 412..412 V -> A (IN REF. 3) .
FT CONFLICT 477..477 M -> I (IN REF. 12) .
FT CONFLICT 513..513 T -> R (IN REF. 10) .
FT CONFLICT 515..515 L -> W (IN REF. 11) .
FT CONFLICT 545..545 G -> R (IN REF. 11) .
FT CONFLICT 551..551 A -> R (IN REF. 10) .
FT CONFLICT 556..556 A -> S (IN REF. 11) .
FT CONFLICT 564..564 T -> N (IN REF. 11) .
FT CONFLICT 570..570 E -> D (IN REF. 11) .
FT CONFLICT 583..583 L -> P (IN REF. 5 AND 9) .
FT CONFLICT 591..591 G -> A (IN REF. 11) .
```

Db 538 VLFATETGKSEALARDLAL-PSYAFNTKVCMEQYKANTLIEBQILLVVTSTFGNDCP 596  
QY 542 DNAKQFVMDLDOASADEVKGV---RYSVFGCGDKMWTYYOKVPAF---IDETLAKGA 594  
Db 597 SNGQTL-----KSLFWMKELGHTFRYAVFGIG-----SSWYPOCFAPHDIDQKLSHIGA 647  
QY 595 ENIADGGEADSDDECTEYEMREHMSDVAATFNLDIENS-----ED 637  
Db 648 SOLAPGEGDELSCQEDAFRSMVQTFR--ACCTFPVRSKHCIOIPKRYTSNATWEPEQ 705  
QY 638 NKSTLSIQFVDSADMDPLAKWH--GAFSTNVVASKELQCPGSARSTR--HLETELPEKAS 693  
Db 706 YKLTQSPESID--LNKALSSIHAKNVFTMRUKSLQNLQSEKSKRTLLVQLTPEGSKRPS 763  
QY 694 YQEGDLGVIPRYVEGIVNREVTARFGLDAS---QOIRLEAEBE-----KLAHLPLAKTV 744  
Db 764 YLPGEHLGIFPGQOTALVQGILERV--VDCSSPDQTVCLEVLDESGSYWVKDRLP---PC 819  
QY 745 SVEELLQY-VELQDPVTRTQIRAMAATVCPPHKVELBALLEKQAYKEQVLAKRLTMLEL 803  
Db 820 SLRQALTYFLDITTPPTQOLHKLARPATEETHRQRLLEALCQPSBYNDMKFSSNPFLFV 879  
QY 804 LEKYPACEMKFEPIALLPSIRPRYVSISSSPRVDEKQASITVSVSGEAMSGYE-YKG 862  
Db 880 LEEPPSLRVPAALFLSQLPLKPRYYSISSQDHTPSEVHLTVAVVYTRTRDQGGPLAHG 939  
QY 863 IASNYLAELQEGDITTCFISTPOSEFTLPKDPETPLIMVPGTGVAPFGFVQAR--KQK 921  
Db 940 VCSWTWINLKPEDVPVPCFVRS-VSGFQLPEDPSQPCILIGPTGIAPFRSFWOQRLHDSQ 998  
QY 922 ECGQSIGEAHLVFGCRSPHEDVLYQEELENAQSEGIITLHTAFSRMPNQKTYVQHME 980  
Db 999 HRGIGKGRMTLVFGCRHPEBDHLQOEMQEMVRKGVLFQVHTGYSRLPKRKYVVDILQ 1058  
QY 981 QD-GKKLIEL--DOGAHYICGDSQMAPAVEATLMKSYADVHQVSEADARLMLOOLEE 1037  
Db 1059 KEIADVFYSVLHGQG-HLYVCGD-VKARDVATTLLKLVAAKLNLSQEVQVEDYFFOLKS 1116  
QY 1038 KGRYAKDWM 1046  
Db 1117 QKRYHEDIF 1125

Search completed: May 29, 2003, 10:04:36  
Job time : 28 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:00:23 ; Search time 99 Seconds  
(without alignments)  
2181.186 Million cell updates/sec

Title: US-10-031-241-35

Perfect score: 5457  
Sequence: 1 TTKEMPOKTFGLKNIPL.....RLWLOQLKRGKRYAKDWAG 1048

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1736.5	31.8	1066	3 Q9Y8G7	Q9Y8G7 fusarium ox
2	1462.5	26.8	1115	3 Q9HGE0	Q9HGE0 gibberella
3	961	17.6	527	16 Q9RD76	Q9RD76 streptomyce
4	773.5	14.2	667	11 Q60451	Q60451 cricetomyce
5	745	13.7	719	10 Q40916	Q40916 pseudotsuga
6	739.5	13.6	692	10 Q9SB48	Q9SB48 arabidopsis
7	737.5	13.5	681	10 Q48937	Q48937 petroselinu
8	734.5	13.5	703	10 Q8X449	Q8X449 triticum ae
9	717	13.1	712	10 Q9A006	Q9A006 populus bal
10	714.5	13.1	692	10 Q39035	Q39035 arabidopsis
11	711.5	13.0	683	10 Q24424	Q24424 papaver som
12	711.5	13.0	692	10 Q9A008	Q9A008 populus bal
13	711	13.0	692	10 Q43235	Q43235 vicia sativ
14	710	13.0	656	10 Q9FTM7	Q9FTM7 triticum ae
15	709	13.0	711	10 Q9S0M3	Q9S0M3 arabidopsis
16	706	12.9	705	10 Q24425	Q24425 eschscholzi

17	705.5	12.9	588	10 Q96561	Q96561 helianthus
18	705	12.9	639	10 Q48938	Q48938 petroselinu
19	702.5	12.9	712	10 Q39036	Q39036 arabidopsis
20	695.5	12.7	704	10 Q04434	Q04434 pisum sativ
21	694	12.7	321	2 Q9ZHK0	Q9ZHK0 rhodococcus
22	691	12.7	712	10 Q9A007	Q9A007 populus bal
23	690.5	12.7	687	5 Q9NKC3	Q9NKC3 bombyx mori
24	689.5	12.6	1147	11 Q9R0W4	Q9R0W4 ratius norv
25	684.5	12.5	662	5 Q09590	Q09590 caenorhabdi
26	681.5	12.5	1311	6 Q9BDH6	Q9BDH6 equus cabal
27	680	12.5	701	5 P91555	P91555 dirosophila
28	680	12.5	736	3 Q9HDC2	Q9HDC2 phanerochae
29	669.5	12.3	1147	11 Q9QW28	Q9QW28 ratius sp.
30	668	12.2	690	3 Q9HGV3	Q9HGV3 phanerochae
31	667.5	12.2	671	3 Q9HFV3	Q9HFV3 rhizopus st
32	665.5	12.2	1145	11 Q8R410	Q8R410 mus musculu
33	661	12.1	1114	4 Q94994	Q94994 homo sapien
34	658.5	12.1	1154	6 Q97604	Q97604 canis famli
35	657.5	12.0	693	3 Q00141	Q00141 aspergillus
36	651.5	11.9	759	3 Q9C498	Q9C498 rhodocoryla
37	650.5	11.9	945	6 Q9N175	Q9N175 ovis aries
38	644.5	11.8	730	3 Q8X1W0	Q8X1W0 coriolus ve
39	636.5	11.7	607	16 Q9K7F6	Q9K7F6 bacillus ha
40	628.5	11.5	605	16 Q32214	Q32214 bacillus su
41	627.5	11.5	506	10 Q96560	Q96560 helianthus
42	617.5	11.3	710	3 Q9PAE2	Q9PAE2 cunninham
43	615.5	11.3	1055	5 Q968Y4	Q968Y4 physarum po
44	605.5	11.1	1206	11 Q9WTX6	Q9WTX6 cavia porce
45	597.5	10.9	1205	6 Q9TX8	Q9TX8 canis famli

## ALIGNMENTS

RESULT 1  
ID Q9Y8G7 PRELIMINARY; PRT; 1066 AA.  
Q9Y8G7  
AC Q9Y8G7;  
DT 01-NOV-1999 (TREMREL. 12, Created)  
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)  
DT 01-MAR-2002 (TREMREL. 20, Last annotation update)  
DE Bifunctional P-450:NADPH-P450 reductase protein (Fatty acid omega-hydroxylase) (P450foxy) [Includes: cytochrome P450 505 (EC 1.14.14.1); NADPH-cytochrome P450 reductase (EC 1.6.2.4)].  
DE CYP505.  
GN Fusarium oxysporum  
OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.  
OC NCBI\_TaxID=5507;  
OX [1]  
RN SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.  
RP STRAIN=MT-811;  
RC MEDLINE=20564350; PubMed=10995755;  
RX Klatzume T., Takaya N., Nakayama N., Shoun H.;  
RA "Fusarium oxysporum fatty-acid subterminal hydroxylase (CYP505) is a membrane-bound eukaryotic counterpart of Bacillus megaterium cytochrome P450BM3.";  
RT J. Biol. Chem. 275:39734-39740(2000).  
RL [2]  
RN FUNCTION, AND SUBCELLULAR LOCATION.  
RP STRAIN=MT-811;  
RC MEDLINE=96271003; PubMed=8830036;  
RX Nakayama N., Takemae A., Shoun H.;  
RA "Cytochrome P450foxy, a catalytically self-sufficient fatty acid hydroxylase of the fungus Fusarium oxysporum.";  
RT J. Biochem. 119:435-440(1996).  
RL  
CC ACTIVITY: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. SHOWS HIGHEST ACTIVITY TOWARD FATTY ACIDS WITH A CHAIN LENGTH OF 12-14 CARBONS. THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450.  
CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2)O;  
CC -1- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) + 2

```

CC FERROCYTOCHROME.
CC -1- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
CC P450 FAMILY.
DR EMBL: AB030037; BAA82526.1; -.
DR HSP; P14779; IBY.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR003097; FAD binding.
DR InterPro: IPR001094; Flavodoxin like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001709; FPN_Cyt_redctse.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD binding; 1.
DR Pfam: PF00258; Flavodoxin; 1.
DR Pfam: PF00175; NAD binding; 1.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
DR Heme; Monooxygenase; Oxidoreductase; Membrane; Electron transport;
KM Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP.
FT DOMAIN 1 480 CYTOCHROME_P450 REDUCTASE.
FT BINDING 481 1066 NADPH-P-450 REDUCTASE.
FT BINDING 407 407 HEME (BY SIMILARITY).
SQ SEQUENCE 1066 AA; 117925 MW; 6B812369C233DBA CRC64;

Query March 31.8%; Score 1736.5; DB 3; Length 1066;
Best Local Similarity 36.8%; Pred. No. 2.5e-100;
Matches 393; Conservative 190; Mismatches 444; Indels 43; Gaps 19;

QY 5 MPOKTEGELNLPNTDKFVQALMKIADLGEIFKEAPGRVTRYSQRLKEACDE 64
DB 7 IPEPGYPLIGNLGEF-TSNPLSDNLRADTYGPIFLRLGAKAPIFVSSSLINVCDE 65
QY 65 SRPKNLSQALKFPRDPAAGDGLFTSWTEKWKWKAHNLILPSECOAMKGYHAMVDIAV 124
DB 66 KRFPKTKSVLSQVREGVHDLPTAFDEBPWGAHRLVPAFPLSLRGFPEMHDIAT 125
QY 125 QLVOKWERNLNDHEIWEDEWTRLTLDITGLCGFNYSRNSFYRDPHFITSWVALDEA 184
DB 126 QLCMKFARHGPRITIDSDNTRIALDLALCAMDFRYSYKSELHFIAMGDFLTES 185
QY 185 MNKLQANPDP--AYDENKRFQEDIKVMNDLVKTIADRKASGEOSDILLTHMLNGKD 242
DB 186 GNR-NRRPFAFNFLYRAANEKFGDIALMKSVADEVAAKAKSDBKDLAAMLVGVD 244
QY 243 PETGEPLDDENIRQITITLHAGHETTSGLSPALYFLVKRPHYLQKAAEAAVLDPV 302
DB 245 POTEKLSDENITQITLITFLHAGHETTSGLSPALYFLVKRPHYLQKAAEAAVLDPV 304
QY 303 PSYQVQOLKVVGNVLEBALMLWPTAPFSLYAKEDPTLVGGEVLEKGDMLAVLIPOLR 362
DB 305 VLVEHLTKLPTISAVLRETLNLSPTIRFGLEALIDDTFLGSKVLYKGEIYALISKHV 364
QY 363 DKTIWGDVEBERER-----FENPSALPQAHFPGNGRACIQOQFALHEATLVLMGM 417
DB 365 DPVYGGADADKFIERMLDDEFARLNKEYPWCWKPFGNGKACIGRPAMGESLAAVYL 424
QY 418 LKHFDFE-DHTNYELDIKETLTLPKRGVVAKSKK-----IPLGSIPEPSTEOS 466
DB 425 FQNFNFTMDPNVLALEIKQITLTKPDHFYINATLRHGWTPELEHVLNAGNATSSSTINI 484
QY 467 AKYRKKAENAHNPLVLVGSNMGTAEGTARLADLAMSGF-APQVATLDSHAGNLR 525
DB 485 KAAINLDAKAGSGKPMALFYSGNSGTALANRLASDPSHGFAITVGPIDQAKQNP 544
QY 526 EGAVLITASYNGHPDPAKQFVMDLQASADEVGVYVYFGCGDKMATTYQKPAFI 585
DB 545 DRPVVITASYEGPSPNAHFIKMMDLDGNDMEKYSYAFACGHDMVTTHIRICLV 604
QY 586 DETLAAGAENIADRGAD-ASDPEGTYEWRB-HMMSDVAAVFNLDIENSEDNKSTLS 643

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DB 605 DSTLEKGGTRVLPMGADADAATDMFSDFEAMBDIVLPGLEKRYKIDSDESGQKLL- 663
QY 644 LQFVDSADAPLAKMHGAFSTNNVASKELQOPASASTRELLELPEASVQSGDHLGVI 703
DB 664 ----VEVSTPKTSLRQVBEALVAEKTLLKSPAK--KHIELQLEPAMTYKAGDYALIL 718
QY 704 PRNVEGIUNVTARFGDLASQOIRLEAEKEKLAHLPLAKTVSVEELIQ-YVELDPVTRT 762
DB 719 PLNPKSTVAVHFRFSPSLAMDSFLKIOSECP--TTLPTNVASIAFDVSAVVELSQPATKR 776
QY 763 QLAAMAKTCPRHVKLELLEKQAYKEQVLAHLRLMLLELKYPCENKFSFETLPL 822
DB 777 NILALAEATDKDCTIOELER-LAGDAQATISPRVSVLLEKFPVVALPISSLMLP 835
QY 823 SIRPRVYSSSPRVDEKQASITVSVSGEAMSGYGEYKIASNYLAELQEGDTTCFIS 882
DB 836 PMRVQYSSISSPPADSKTLTYSLDASLSGGQGHGVAVANFLSHLYAGDKLHVSVR 895
QY 883 TPQSEFTLPKDP--TPLINVGPGTGAFFRGVQARKQLEQOSLGEAHLFYGCSPHE 941
DB 896 ASSEAFPLPEDAEKTPITCVAAGTGLAPLFGFIOERAAMLAARTLAPALLFGCRNPEI 955
QY 942 DLYQELNLAQSEGITTLTATSRMPNOKP--TYQVHNEQDQKLIELLDGAHNYIC 999
DB 956 DDLAEFEFERKMGAVDVARAVSRATDKSEGGKYVDROYHPRADVFKWDDQAKVFC 1015
QY 1000 GDGSONAPAVE-----ATLMKSYADVHQVSEADARLTLQOLEKGRYAKDWM 1046
DB 1016 G-SREIKAYEDVCVRLAIEKAQONGRDVTEBAAKMFERSRNE-RATVTF 1065

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RESULT 2
Q9HGE0 PRELIMINARY; PRT; 1115 AA.
AC Q9HGE0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE FumGp.
GN FumG.
OS Gibberella moniliformis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Nectriaceae; Gibberella.
OX NCBI_Taxid=117187;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M-3125;
RA Proctor R.H.; Seo J.-A.; Plattner R.D.;
RT "Characterization of four clustered and coregulated genes associated
with fumonisin biosynthesis in Fusarium verticillioides."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL: AF155773; AAG27132.1; -.
DR HSP; P00386; J992.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR003097; FAD binding.
DR InterPro: IPR001094; Flavodoxin like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001709; FPN_Cyt_redctse.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD binding; 1.
DR Pfam: PF00258; Flavodoxin; 1.
DR Pfam: PF00175; NAD binding; 1.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
KM Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 1115 AA; 123276 MW; 56CD2B947AE86C25 CRC64;

Query Match 26.8%; Score 1462.5; DB 3; Length 1115;

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QY 56 RLKACDESFDPKLSQALKFVDFAGDGLFTSMTEKMKKANKNILLPFSQOAMKGY 115
D 82 ALAADLADDEARFAGHVGIVGANLRVAGDGLFTAYNHENPMQHLADVLAPFSEANAGY 141
QY 116 HAMVNDIAVOLVOKERLNAD-EHI EYEDMTRLTLDTLGLCGFNENRNSYRDQPHPI 174
D 142 HVMMLDVAAARLTGMHDLAEASGRAVDYGDWTKLTLETIARTGFGHFGSFEERSLHPFV 201
QY 175 TSMVRLADEAMNKLOAN----PDDP--AYDENKKOFOGDIKVMNDIVDKIADSKA----- 225
D 202 TAMVGTLCYA---QRLNTVPAPLAPMLLRDASRNADIAHLKRYDDLVERRANGCT 257
QY 226 -----SGEOSDILLTHMLNGKDPETGEPLDENIRYOIITFLIAGHETSGLSFALYFL 280
D 258 GCGTSGSGSGDLDRLMLETNHPRTGERLSPQVNRQVITFLVAGHETSGLSFALHYL 317
QY 281 VKNPHVLQKAAEAPARLVLD-PVPSYKOVKOLKTYGVNLALMLPAPAPSLYAKEDT 339
D 318 AQHBDVAAARAEVDRVWGDTAPGVEQVAKLRVVRRLDESRLMPTAPGFAREAREDET 377
QY 340 VLGGSEPLEKGDLMVLIPOLHRDKTIWGDVSEPRPRENPAIPQ--HAFKPFNGQ 397
D 378 VLGGTHPRRGAAMLVLGMLHRDEYVGADAEPRDPFPAKAVRSAPHTFERPGTGA 437
QY 398 RACIGQOFALHEATLVLGMLKHFDFEDHTNVELDIKETTLLKPEGFVAKAKSKIPLG 457
D 438 RACIGRQFALHEATLVGLLRREYELREPEGRRLRVTRELLTMEGLHLHLVR---TAA 494
QY 458 IPSPSTEOSAKVRKKAENAHNT 481
D 495 APAPGRRTAAPGAADADAGTVSAP 518

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## RESULT 4

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ID 060451 PRELIMINARY; PRT; 667 AA.
AC 060451;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE NADPH-cytochrome P450 oxidoreductase.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=GOLDEN;
RC Ohguya S., Gada T., Hoshino T., Shinzaki N., Kametaki T.;
RT "High-red yeast, construction of a novel strain of Saccharomyces
RT cerevisiae stably exerting high activity of hamster cytochrome P450
RT reductase.";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D83230; BA11856.1; -.
DR HSSP; P00388; IAWO.
DR InterPro; IPR003097; PAD binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001433; FPN_cyt_redctse.
DR Pfam; PF00667; FAD binding 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KM NADP.
SQ SEQUENCE 667 AA; 75850 MW; 2023F43DF4C1EF07 CRC64;

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Query Match 14.2%; Score 773.5; DB 11; Length 667;  
 Best Local Similarity 32.1%; Pred. No. 3.9e-40;  
 Matches 210; Conservative 117; Mismatches 260; Indels 67; Gaps 25;

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QY 444 FVYAKSKKIPLG---IPSPTEOSA--KVRKKAENAHNTPLVLYSGNMGTAEGRAR 498
D 31 FIRKKKEVEPESKIQIOTATPSVKESFVEKMKKTGN-----IIVYGSQTGAEEFAN 85
QY 499 DLADIAMSKFAPQVATLDSH---AGNLP--EGAVLIYASY-NGHPDNKAPVDWL 551
D 86 RLSDKARHYRGMSADPEEYDLADLSLPEIKSLVFCMATYGEEDPDNDQFDYDWL 145
QY 552 DQASADKVKVRYSVFGCGKNNATYQKVP---FIDETLAKGAEINIDRGADSD 608
D 146 QETDVD-LTGKFAVFGNGK---IYENNAKGYVDQLBOLGAORITELGIDDDGN 200
QY 609 FEGTYEEMRHMMSDYAAYENLDIENSEDNKSTLSL--QFVSA----ADMPKXN-- 659
D 201 LEBDFIWRQFPNPAVECFEFGVEATGESIRQVELLVHEDIDDAKAYTTEMGRKLYEN 260
QY 660 -----GAFSTNVYASKELQOPGARSIRHLEI--PREASTQSGDHGVIPTNYEGT 710
D 261 QKPEFDANKPEFLAATVTRNLNQ--GTERHLMHLELIDSKIRYESGDHVAVYPADSTL 319
QY 711 VNRVTAFFGLDASQOI---RLBAEEKLAHLPLAKTVSVELQYVELQDPVTRTOLRAM 767
D 320 VNOIGETLGADLVVMSLNNLDESSNKAPPPCPTTIRT-ALTYLDTNP-PRTNVLYE 377
QY 768 AAKTVCP-----HKVELALKEQAYKEQVLAKRLTMLELEKYPACEMKTESEFALL 821
D 378 LAQYASPESSQEOQLHKWASSGEGKELYLSMVVEARHIALIADYPSLRPIDHCELL 437
QY 822 PSIRPRYYSISSPRDEKCASTVSVSGEAMSGEYGIASNYL-AELQSGDT---- 876
D 438 PRLQARYSIASSSKVAPNSVHICAVAVEAKSGRVN-KGVATSWRAKEPGENGRRA 496
QY 877 -ITCFISTPQSEFTLPDREPLIMVPGTGVAPRFGFVARQOLKEQGSLSGAHLVFG 935
D 497 LPMVEVR--KSQFRLPKSVTPVIMVGGTGLAFPMCFIOERAMLRQGEVGETLLYYG 554
QY 936 CRSPHEDLYQOELENAQSEGIIT-LHTAFSRMNPQPTVYQVHMEQDGKLTLELDQ-G 993
D 555 CRSDDELYLVRELARHKGALQUNVAFSR-EQAHKYVVQHLLKDRHMLWLHIEGG 613
QY 994 AHFYICDGSQMAPAVEATLMKSYADVQVSEADARIMLOQLBEKGRYAKDWA 1047
D 614 AHIVCGDARNMAKDVQNTFYDIVAERGPMEHAQADVVKLMTKGRYSIDVWS 667

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## RESULT 5

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ID 040916 PRELIMINARY; PRT; 719 AA.
AC 040916;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4).
GN CPRL.
OS Pseudotsuga menziesii (Douglas-fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pseudotsuga.
OX NCBI_TaxID=3357;
RN [1]
RP SEQUENCE OF 1-44 FROM N.A.
RA STRAIN=(MIRB) FRANCO; TISSUE=SEEDLING;
RC Triabarger T.J., Misra S.;
RT "The molecular characterization of a set of cDNAs differentially
RT expressed during Douglas-fir germination and early seedling
RT development.";
RL Physiol. Plantarum 95:456-464 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=(MIRB) FRANCO; TISSUE=SEEDLING;
RA Triabarger T.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

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592 AIOKSGEKLPAVLFVFCGRNRQMDYIYEDELKSYVNGVLTETLVAESR-EGATKEVYQH 650
Oy 978 VMEDEGKKLIELDQGHAFITCGGSGOMAPAVEYTLTKSYADVQYSEADRLMLQQLFE 1037
Db 651 KITEKSGYVNIWLLAQGGYLVYCGAKAKMARDVHTLHLSIVQESVSTSAEATVKQLQT 710
Oy 1038 KGRYAKDVM 1046
Db 711 EGRYLDVM 719

RESULT 6
09SB48
ID 09SB48 PRELIMINARY; PRT; 692 AA.
AC 09SB48;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2002 (TREMBlrel. 20, Last annotation update)
DE NADP-FERRIHEMOPROTEIN reductase ATPL1 (EC 1.6.2.4).
GN P22K18.280 OR AT4G24520.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Wedler H., Wambutt R., Hohelsel J., Mewes H.W.,
RA Mayer K.F.X., Schueller C.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsids sequencing project;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Wedler H., Wedler E., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsids sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Southgate A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Chouk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinzaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035356; CAA23011.1; -
DR EMBL; AL161561; CAB79362.1; -
DR EMBL; AY054668; AK96879.1; -
DR HSSP; P00388; IAMO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FEN_cyt_redctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1.
DR Pfam; PF00258; Flavodoxin; 1.
DR Pfam; PF00175; NAD_binding_1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FMCR.
KW Oxidoreductase.
SQ SEQUENCE 692 AA; 76765 MW; 7DD77E418CF2FA6 CRC64;

Query Match 13.6%; Score 739.5; DB 10; Length 692;
Best Local Similarity 29.6%; Pred. No. 5,7e-38;
Matches 196; Conservative 120; Mismatches 257; Indels 89; Gaps 19;
441 PEGFVFAKSKKIPUGIGIPSPBTEQASAKVRKKAENAHNPPLVLVYSGNMGTAGTARDL 500

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Db      64 PKSLMAKDEDDDLG-----SKRTVSIFFGQTSTAAGFAVAL 103
Qy      501 AD--IAMSKEGPAVATLDHSHAGN-----LPREGAVLITASY-NGHPDNAAQFVDM 550
Db      104 SEELKAREKAAVVIDDDYAADDDQYBEUKKETLAFVATITGDEPDMNARFKW 163
Qy      551 LDQASADEVK--GVRYSVGGCGDKMATTYQVPAFIDETLAAGAENIADRGADASDD 608
Db      164 FTEENERDKLQOALAYGFALGNROY--EHFNKIGIVLDEELCKGAKRLIEVGLDDQOS 222
Qy      609 FEGTYEERHEHMDVAAYFNL--IENSEDNKS-----TSLQ 645
Db      223 IEDFNNAKESLWSE-----LDKLKDEDKSAATPYTAVIPYRVVTHPRFTTQKSM 276
Qy      646 FVDSADMPFLAKMGAFSTNVVASKELQPGSARSTRHLEIPEKA-SYOEGBHLGVI 704
Db      277 ESNVANGNTTIDIHPCRVDAVQKELHTHSDNSCHLEPDISRTGITTYGDBVGYA 336
Qy      705 RNYEGIVNRVTARFGLDASQOIRLEAEEKLAHLPLAKTVSV-----EELLQYVEL 755
Db      337 ENHVEIVEAGKLLGHSIDLVFISHADKEDGS--PLESAVPPPPPGCTTGLGARVADL 394
Qy      756 QDPYTRQOLAMAAKTVPKPKVELEALLE--KOAYKEOVLAKRLTMLLEKYPACEM 812
Db      395 LNPBKSLVALAVALATEPSEAEKIKLITSPDGDEYSQWIVASQRLIEVMAAFPSAKP 454
Qy      813 KFSEFI-ALLPSIRPRYSISSPPRDEKQASITVSVSGEAMSGYGEKGIASNYL--- 868
Db      455 PLGFYFAIARLQPRYYSISSPRLASRVHTSALVYGPPTG-RHKGVCSITMKNNA 513
Qy      869 --AEOGDTITCFISTQSEFTLPKDPETPLIMVGTGVAAPRGVQARQOLKEGO 925
Db      514 VPAKSHESGAPFIRA--SNFKLPSPNPTPIVWVGSGTGLAPRGFLQGRMALKEDE 571
Qy      926 SLGSAHLVFGCRSHEDLYOELENAQSEGIT--LHTAFSRMPQPTTYQVHMEODGK 984
Db      572 ELGSSLFFGGRNOMDPIYEDELNPFVQGVISELIVAFSREGAQ--KEYVQHKMEKXA 630
Qy      985 KLIELDGAFFYICGDSQNAAPAVEATIMKSYADVHGVSEADARLMLQLEKGRYAKD 1044
Db      631 QVMDLKEGVLVYCGDAKGAARDVHRTLHTIVGEOBVSSEBALVKKLQTEGRYLND 690
Qy      1045 VW 1046
Db      691 VW 692

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RESULT 7

048937 PRELIMINARY; PRT; 681 AA.

AC 048937; TREMBLrel. 06. Created)

DT 01-JUN-1998 (TREMBLrel. 06. Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20. Last annotation update)

DE NADPH cytochrome P450 reductase (EC 1.6.2.4).

GN Petroselinum crispum (Parsley) (Petroselinum hortense).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.

OX NCBI\_TaxID=4043;

RN

RP SEQUENCE FROM N.A.

RX MEDLINE=98070859; PubMed=9405720;

RA Koopmann E., Hahlbrock K.,

RT "Differentially regulated NADPH-cytochrome P450 oxidoreductases in

RL Parsley."

DR EMBL; AF024634; AA897736.1; -.

DR HSSP; P00388; IJMO.

DR InterPro; IPR003097; FAD\_binding.

DR InterPro; IPR001094; Flavodoxin\_like.

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DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FEN_cyt_redctase.
DR InterPro; IPR001433; Oxid_FAD/NAD (P).
DR Pfam; PF00667; FAD_binding_1.
DR Pfam; PF00258; Flavodoxin_1.
DR Pfam; PF00175; NAD_binding_1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR Oxidoreductase.
KW SEQUENCE 681 AA; 75674 MW; C67AD080E8BAE0F6 CRC64;

Query Match 13.5%; Score 737.5; DB 10; Length 681;
Best Local Similarity 30.7%; Pred. No. 7.4e-38;
Matches 200; Conservative 104; Mismatches 275; Indels 73; Gaps 18;

Qy 449 KSKKIPGGIPSPSTEQSAKVRKKAENANTPLVLYGSGNMGTAEGBTARDLADIAKSG 508
Db 49 KSVPEPLVLPKYEIEBEVDGKK-----VTYVFGITGTABEFAPAEAEARARY 100
Qy 509 FAP--QVATLDSHA-----GNLPREGAVLITASY-NGHPDNAAQFVMDLQA--SA 556
Db 101 EKAFRVVDDDYAADEEYEAKEKESFAFFELATYGDGEPTDMNARFYKWFSEGEKG 160
Qy 557 DEVKGVYVSPGCGDKMATTYQVPAFIDETLAAGAENIADRGADASDDDEGTYEEN 616
Db 161 DWNKQLYGVFGIGNROY--EHFNKIAKVDDGLADQAKRIVEGMDDDQCIEDDTJAW 219
Qy 617 REHMSD-----VAAYPNLDIENSEDNKSTLSLQFVDSAA 651
Db 220 RELVWPELDLKLDEDDTSAATPYTAVALERYVVVDQDLTALDLRSLSTONGHTYDA- 278
Qy 652 DMLAKMGAFTNVVASKELQPGSARSTRHLEIPEKA-SYOEGBHLGVIIPRNYEG 710
Db 279 -----QHPERS-SVAAKKEHLKPADSRSCIHLEPDISHTGLAYETGDHGVYCNELVEI 331
Qy 711 VNRVTARFGDASQOIRLEAEEKLAHL-----PLAKTVSVBELLYVELDQVTRTQ 763
Db 332 VEEAEKLLGQNPITYFSVHLDDEGTPLTGSLPPPPCTVBSAALKYADLLSSPKSA 391
Qy 764 LRAVAATVCPKPKVELEALLE--KOAYKEOVLAKRLTMLLEKYPACEMKFSEFIRA- 819
Db 392 LIALAAASPTEDRLRLASPGKDEYAGWVVASHSRLIEVLAEPSPAKPLGVFFAS 451
Qy 820 LLPISIRPRYSISSPPRDEKQASITVSVSGEAMSGYGEKGIASNYL--AEOG-D 875
Db 452 VAPRLQPRYYSISSPPRDEKQASITVSVSGEAMSGYGEKGIASNYL--AEOG-D 875
Qy 876 TITCFISTPQSEFTLPKDPETPLIMVGTGVAAPRGVQARQOLKEGOSLGEAHLYFG 935
Db 511 CSWAPIFVRQSNFCLPSDTPVPIIMIGPGTGLAPFRGLQERQALDAGAEIGTAVLYFG 570
Qy 936 CRSPHEDLYOELELN--AQSEGITLHTAFSRMPNQPTTYQVHMEODGKLIJELDOGA 994
Db 571 CRNENLDFIYEDLNKVESGISELIVAFSR--BGPKEYVQHKMLQKAEIMWLJESGA 629
Qy 995 HFYICGDSQNAAPAVEATIMKSYADVHGVSEADARLMLQLEKGRYAKDVW 1046
Db 630 YIVYCGDAKGAARDVHRLHTIAQEGALDSSAESVVKULQMTGRTYLRDVW 681

```

RESULT 8

08VX49 PRELIMINARY; PRT; 703 AA.

AC 08VX49; TREMBLrel. 20. Created)

DT 01-MAR-2002 (TREMBLrel. 20. Last sequence update)

DE 01-JUN-2002 (TREMBLrel. 21. Last annotation update)

DE Cytochrome P450 reductase (EC 1.6.2.4).

GN

OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Triticum.





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Db 601 GCRRNRKDFIYEDLNPFVSGALSELVAFNR-EGPTKEYVQHKMOKASDINNMISQC 659
Qy 994 AHFYICGDSQMAVAVENTLMKSYADYHOVSEADARLMLQOLEEKGRYAKVM 1046
Db 660 GYLVCVDGAKGMADVHRALHTTVIQEOGSLDNKSTESVSLQNNGRRLRVW 712

RESULT 10
Q39035 PRELIMINARY; PRT; 692 AA.
ID Q39035
AC Q39035;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE NMDPH-ferritinoprotein reductase.
GN ATR1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEYNH; TISSUE=SEEDLING;
RA Mignone-Vieux C., Kazmaier M., Lacroite F., Pompon D.M.;
RL Submitted (May-1992) to the EMBL/Genbank/DBJ databases.
DR EMBL; X66016; CAA46814.1; -.
DR HSBP; P00388; IAMO.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_reductase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD binding; 1.
DR Pfam; PF00258; Flavodoxin; 1.
DR PRINTS; PR00175; NAD binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
SQ SEQUENCE 692 AA; 76768 MW; 5E0216F008B5D49E CRC64;

Query Match 13.1%; Score 714.5; DB 10; Length 692;
Best Local Similarity 29.2%; Pred. No. 2.1e-36;
Matches 193; Conservative 119; Mismatches 261; Indels 89; Gaps 19;

Qy 441 PEGFVRAKSKKIPLGIPSPSTQSAKVKAKAENANPTPLVLVYGSNMGTAEGTARDL 500
Db 64 PKSLMADDEDDDLG-----SKTNVSIFFGTQTATGSAKAL.103
Qy 501 AD-IAMSKGAPQVATLDSHAGN-----LPREGAVLIVTASY-NGHPDPAKQFVDM 550
Db 104 SEETKAREKAAKVYDLDYAADDDQYEELKKETLAFCAATYGDSEPTDNARFSKW 163
Qy 551 LDOASABEVK--GVRYSFGGCDKMAATYQKVAFIDETLAAGAENIADRGADASDD 608
Db 164 FTEENEDIKLOQLAYGFALGNROY-EHFNKIGIVLDEELCKGAKLIEVGLDDQDS 222
Qy 609 FEGYEEMREHMMSDVAAYFNLD-IENSEDNKS-----TLSTLQ 645
Db 223 IEDFPMKESLWSE-----LDKLLKDEDDKSVATPTVAVPEYRVTHDPRTTQSKM 276
Qy 646 FVDSADWPLAKMHGAFSTNVVASKELQPGSASRTRHLELPKEA-SYOGDHLGYTP 704
Db 277 ESNVANGNTTIDIHPRCVDVAVOKEHLTHESDRSCILBEDISRTGITETGHDVGYA 336
Qy 705 RNYGCIYVRVTAARGLDASQOIRLEAEKEKLAHPLAATVSV-----ELLQYVEL 755
Db 337 ENHVEIYEBAKGLGSHLDLVSFHADKEDS--PLESAVPPPPPGCTLTGRLARYADL 394
Qy 756 QDPATRTQLRMAKATVCPKHVELEALLE---KOAYKEOVLAKRLTMTLELKYPAECM 812
Db 395 LNPFRKSLVALAAVATPSEAEKULKHLTSPDGADYSQWIVAGORSILLEVMAAFPSAKP 454

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Qy 813 KESEFT-ALLPSIRPRYSSSPRDEKQASTVSVSGEAMSGCEYGIASNYL--- 868
Db 455 PLGVFFAALIPRLQPRYSSSCODWAPSRVHTSALVGPPTGT-RHHGVCSTWAKNA 513
Qy 869 ---AEIQEGDTICPSTPQSEFTLPKDPETPLIMGPGGVAPFGGVQARQOLKEQG 925
Db 514 VPAKSHESGCAFTIFIRA--SNKFLPSNPSTPIVMGPGTGLAPFRGFLQERNALEDGE 571
Qy 926 SLGEAHLVFCGRSPHEDYLYQEELENAQSEGIIT-LHTAFSRMNPQPKTYQHVMEQDGK 984
Db 572 ELGSSILFFGCRNRQMDFIYEDLNPFVSGALSELVAFNR-EGPTKEYVQHKMOKAA 630
Qy 985 KLIELDQGNHFIYICGDSQMAVAVENTLMKSYADYHOVSEADARLMLQOLEEKGRYAKD 1044
Db 631 QVMDLKEEGYLYCGDAGKGMADVHRALHTTVIQEOGESSSEAEALVKRLQTEGRYLRD 690

Qy 1045 VM 1046
Db 691 VM 692

RESULT 11
Q24424 PRELIMINARY; PRT; 683 AA.
ID Q24424
AC Q24424;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE NMDPH-ferritinoprotein oxidoreductase (EC 1.6.2.4).
OS Papaver somniferum (Opium poppy).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Papaveraceae; Papaver.
OX NCBI_TaxID=3469;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98096363; PubMed=9434750;
RA Rosco A., Pauli H.H., Priesner W., Kutchan T.M.;
RL "Cloning and heterologous expression of NMDPH-cytochrome P450
RT reductases from the Papaveraceae."
RL Arch. Biochem. Biophys. 348:369-377(1997).
DR EMBL; U67185; AAC05021.1; -.
DR HSBP; P00388; IAMO.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_reductase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD binding; 1.
DR Pfam; PF00258; Flavodoxin; 1.
DR Pfam; PF00175; NAD binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
SQ SEQUENCE 683 AA; 75888 MW; E07BD5E5EADBE002 CRC64;

Query Match 13.0%; Score 711.5; DB 10; Length 683;
Best Local Similarity 30.3%; Pred. No. 3.2e-36;
Matches 191; Conservative 113; Mismatches 263; Indels 63; Gaps 20;

Qy 470 VRKAENANPT---LLVLVYGSNMGTAEGTADLAD-IAMSKGAPQVATLDSHAG-- 521
Db 64 IDKEEIEIEVDPGIKLTIFFGTGTGTAEGFAKALAEIKAKYKAVKVVKVDVDDYAAD 123
Qy 522 ---LPREGAVLIVTASY-NGHPDPAKQFVDMDO--ASADDEVGVGVYSGCGDKN 573
Db 124 DQYEELKKKESLVFPMVATYGDSEPTDNARFYKFTQEHREGSMQLQTLVGVGLGNRO 183
Qy 574 MATTYQVPAFIDETLAAGAENIADRGADASDDEGTYEEMREHMMSD----- 623
Db 184 Y-EHFNKIVADVDEQLGQAKRIYVGLGDDQCIEDPTARRELLMTLDDQLKXEDA 242
Qy 624 -----VAAYFNLDIENSEDNKSTLSLQFVDSA-ADWPLAKMHGAFSTNVVASKELQ 674

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Db      243 ABVATPYIAITVBERVVIHETVAALDDHINTANGDVAFDILHPC-RTTVAQORELHK 301
Qy      675 PGASARSTRHLEIEP--KEASYQOEGDHLGVI PRNVEGIVNVTARFG--LDASOOIRLEAE 731
Db      302 PKDRSGCIHIEFDISSSSLYTEGDHGVYAENDEVEERAGKLLGGPDLPLPSIHDK 361
Qy      732 EEKLAHLPLAKTVSV-----EELLQYVELQDPVTRTQOLRAMAKTVCPPHKYLEA 782
Db      362 DGS-----PGSSLPPEPPGPGCTLRALSALARYADLINPRKASIALIASHAASVPSAEIRLF 417
Qy      783 L-----LEKQAYKEQYLARLIMLELEKYPACEMKFSFEI-ALLPSIRPRYSSISSSRVD 838
Db      418 LSSPLGKNEYSKMWVGSORSLLEIMAEFPSPAKPPLGVFAAVARLPRRYSISSSPKA 477
Qy      839 EKASITVSVSGEAMSGYGEYKGIASNYLAELQEGDT-ITCFISTQSEFTLPKDETP 897
Db      478 PSKIHVTCALVYGOSPTG-RVHRGVCSTWKKHAPQDSMAPIFRT--SNFKLPADSTP 534
Qy      898 LIMGPGTGVAPFRGFVQARQOLKEGOSLGEAHLVFCRSPHEDYLYOELENAQSEGI 957
Db      535 IIMVPGTGLAPFRGFLQERWALKENGAGPAVLFGCRNRNMDFIYEDLNNFVERGV 594
Qy      958 IT-LHTAFSMPNPKTYVQVHWEQDGKLIELLDQAHFYICGDSQMAPVEATLMKS 1016
Db      595 ISELVIAFSR-EGEKKEYVGHKMEKATDWNVVISGDDYLYVCGADAKMARVHRTLHTI 653
Qy      1017 YADVQVSEADARLMLQOLEEKGRYAKDW 1046
Db      654 AQOEGPMESSAAEAAYKQLOVEERYLRDW 683

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## RESULT 12

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Q9AU08 ID Q9AU08 PRELIMINARY; PRT; 692 AA.
AC Q9AU08;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, last sequence update)
DE NADPH-cytochrome P450 oxidoreductase isoform 1.
OS Populus balsamifera subsp. trichocarpa x Populus deltoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Salicaceae; Populus.
OX NCBI_TaxId=3695;
RN [1]
RP SEQUENCE FROM N.A.
RA Ro D.-K., Douglas C.;
RT "Functional characterization of cytochrome P450 reductase from the
RT hybrid poplar (Populus trichocarpa x P. deltoides).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF02496; AAK15259.1; -.
DR HSSP; P00388; 1A0.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding.1.
DR Pfam; PF00258; Flavodoxin.1.
DR Pfam; PF00175; NAD_binding.1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
SQ SEQUENCE 692 AA; 76425 MW; 7AA8CC7AB3C984D9 CRC64;

```

## Query Match

Best Local Similarity 13.0%; Score 711.5; DB 10; Length 692;

Matches 199; Conservative 110; Mismatches 252; Indels 127; Gaps 20;

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Qy      431 LDIKETLTLPEGVVAKSKKIPISSTQSAKKYRKAKENAHNTPLVLVYGSNM 490
Db      60 LVVPKLSLIDK-----EDSEALGG-----KTKVTIFYGTOT 92

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Qy      491 GTAEGTARLAD--TMSKGFAPQVATLDSHA-----GNLPRGCAVLITVASY-NGHP 540
Db      93 GTAEGFKAALAEVVKARYEKAAYKVFDDDYAMEDDQYEEKLKKETLALFMVATYDGED 152
Qy      541 PDNAKQFVMDASADSV--KGVRSYVFCGCGKMMATTYOKYPAFTIDETLAKGAEINIA 598
Db      153 TDNAARFYKFTENGNGIGWLQOLSYVFLGKROY-EHFNKAKVLDLTYQGGKRLV 211
Qy      599 DRGEADASDDEFEYTEEMREHMMSDVAAYFNLDIENSEDNKSTLSLOFVDSADMPLA-- 656
Db      212 PVGLGDDQDCEIDDFSAKKEFLWPELD-----QLNDEDDVNAFSPYTAIPEYLVIH 266
Qy      657 -----KKGAFSTNVASAKLQOPGASRSTRHLEIEPKA-SY 694
Db      267 DPSIISVEDKFSNLIANGVNSFDIHPCRVVAQKELHVAESDRSCIHLEFDITGITY 326
Qy      695 QEBDHLGVI PRNVEGIVNVTARFGDAQOQIRLAEBEELALPLAKTVSV----- 747
Db      327 ETGDHLGVYAENSDEVE-----EAGLIDKPLDLLFSIHADNEDGT 368
Qy      748 -----EELLQYVELQDPVTRTQOLRAMAKTVCPPHKYLEALB---K 786
Db      369 AIGSSLPPEPPGPGCTLHTALACYADLISPKKALALALAAHASEPSEADRLKFLSSPQK 428
Qy      787 QAYKEQYLAKRLTMELEKYPACEMKFSFEI-ALLPSIRPRYSSISSPRVDEKQASIT 845
Db      429 NEYSHWMAVSQRLLEVMAEFPSSKPLGIFFAVAAPRIQRYSSISSSPRYPNRVHT 488
Qy      846 VSVSGEAMSGYGEYKGIASNYL---AEQEGTITCF---ISTPSEFTLPDPETPLI 899
Db      489 CALVGPPTPG-RIHNGVCSWKKNAVPLEK--SYCSWAPIFRTSNFGLPADSTPIT 545
Qy      900 MVPGTGVAPFRGFVQARQOLKEGOSLGEAHLVFCRSPHEDYLYOELENAQSEGIIT 959
Db      546 MVPGTGLAPFRGFLQERWALKENGAGPAVLFGCRNRNMDFIYEDLNNFVERGV 605
Qy      960 -LHTAFSMPNPKTYVQVHWEQDGKLIELLDQAHFYICGDSQMAPVEATLMKSYA 1018
Db      606 ELIVASREBPQ-KEYVGHVMDVRAAEIWTIISQGVFYVCGADAKMARVHRTLHTI 664
Qy      1019 DVHQVSEADARLMLQOLEEKGRYAKDW 1046
Db      665 EGGGLDSKTESWVKLQMEGRYLRDW 692

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## RESULT 13

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ID Q43235 PRELIMINARY; PRT; 692 AA.
AC Q43235;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, last sequence update)
DE NADPH-ferritinoprotein reductase (EC 1.6.2.4).
OS Vicia sativa (Spring Vetch) (Tare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxId=3908;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VAR. LOLITA; TISSUE=SEEDLING;
RA Benveniste I., Beque-Klim C., Lesot A., Hasenfratz M., Duret F.;
RT "Isolation and characterization of a cDNA encoding an NADPH-cytochrome
RT P450 reductase from Vicia sativa.";
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z26252; CAAB1211.1; -.
DR HSSP; P00388; 1J92.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding.1.

```

DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00175; NAD binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FENCR.  
 KM NADP: Oxidoreductase.  
 SQ SEQUENCE 692 AA; 76912 MW; 49CB4AEC611BB99 CRC64;

Query Match 13.0%; Score 711; DB 10; Length 692;  
 Best Local Similarity 28.4%; Pred. No. 3.5e-36;  
 Matches 198; Conservative 120; Mismatches 287; Indels 92; Gaps 21;

QY 406 ALHATVILGMLGHPEDHTNELDKETLTKPESFVVKASKIPLGIGSPSTEQ 465  
 DB 32 ATTSAAVILGLV--FLMRKSPDRSRELPAIVK--FTYKHDDDEV----- 76  
 QY 466 SAKYRKAEVNAHTPLVLVYGSNMGTASTADLAD--IAMSGFAPQVATLDSA--- 520  
 DB 77 -----DRGITKTVTFYGTGTGTAGTAEKAKLAIEIKARYEKAVVKKVDMMDYALDD 126  
 QY 521 ----GNLPREGAVLIVTASY--NGHPDNKAKQFVMDLQASADE--VKYRVSVFGGDK 572  
 DB 127 DQYBEKLKKEKTLVFFMLATYGDGEPTDVAARFYKMFTEGKEEGTWMQLTYGVFALGNR 186  
 QY 573 NMATYQKVPFIETLAKAENIADRGENDASDDEPGTGEEMREHMSDVAAVFNLDI 632  
 DB 187 QY--EHFKIKGIVDEDLTEOGAKRLVPVGLDDQSIEDENAKETLMPELD-----QL 240  
 QY 633 EENSEDKSTLSLOFVDSADWPLA-----KMHGAFSTNVVAS 669  
 DB 241 LRDDDDVNTASTPTTAISERVVITHPTVSPYENHPNVANGAVPDIIHPKAVNNAVR 300  
 QY 670 KELQOPGASARSTRHLELP--KEASYOEGHGLVYPRNYEGIVNRVTARFGLDASQOIRL 728  
 DB 301 RELHKPOSDRSCIHLEFDLSGTGTETGHDVGYAENCDETEBEAGKTLGOSLDLFLSL 360  
 QY 729 EAEBEKLAHL-----PLAKTVSVBELLO--YVELODPTRTQDLAMAKTVCPHXYELE 781  
 DB 361 HTDEDETSLSGSLPPRPGPCVTRTALACYADILNPRKKAIVALLAAHSEPEABRLK 420  
 QY 782 ALLE---KQAYKEOVLAKRLTMLLEKELPACEMKFESEFI--ALLPSIRPRYSSISSPRV 837  
 DB 421 FLSPQSGKDEYSKKNVSGSLLEVMADFPSPAKPLVGFPAALPRLOPRYSSISSPR 480  
 QY 838 DEKQASITVSVSEANSGYGEVKGIAVNYLAEL---QEGDTITCFISTPQSEFTLPKD 893  
 DB 481 APQVHTVTCALVEGPPTG--RIHKGVCSITWKSATPLEKSHDCSRAPFIFRPSFKLPAD 539  
 QY 894 PETLIVNGPCTGVAPRPGVQARKQKQOSIGEAHLVFGCRSPHEDVLYQSELENAQ 953  
 DB 540 HSITIVNGPCTGVAPRPGVQARKQKQOSIGEAHLVFGCRSPHEDVLYQSELENAQ 959  
 QY 954 SEGIIIT-LHTFASMPNQPTTYVOHVMQDGKLIILLDGAHFYICGDSQMAPAVEAT 1012  
 DB 600 QQGAISELIVAFSR--EGPEKEVYQHKMDKAEYMLSLISQSGIYVCGDAGKAKRDVHRS 658  
 QY 1013 LMKSYADVHQVSEAD---ARLMLQOLEKGRYADVW 1046  
 DB 659 L---HTIVQOQENADSSKAEATVKKLQWIDGRYLRDVW 692

RESULT 14  
 ID Q9FWM7 PRELIMINARY; PRT; 656 AA.  
 AC Q9FWM7;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE NADPH-cytochrome P450 reductase (fragment).  
 OS Triticum aestivum (wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticaceae; Triticum.  
 NCBI\_TaxID=4565;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, DARIUS;  
 RX MEDLINE=20322901; Pubmed=10864454;  
 RA Batard Y., Hehn A., Nedelkina S., Schalk M., Pallett K., Schaller H.,  
 RA Werck-Reichhart D.,  
 RT "Increasing expression of P450 and P450-reductase proteins from  
 RT monocots in heterologous systems."  
 RL Arch. Biochem. Biophys. 379:161-169(2000).  
 DR EMBL; AF12610; AAC17471.1; "  
 DR HSSP; P00388; 1AM0.  
 DR InterPro; IPR003097; FAD binding.  
 DR InterPro; IPR001094; Flavodoxin-like.  
 DR InterPro; IPR001226; Flavodoxin.  
 DR InterPro; IPR001709; FPN Cyt. reductase.  
 DR InterPro; IPR004433; Oxid. FAD/NAD(P).  
 DR Pfam; PF00258; FAD binding; 1.  
 DR Pfam; PF00258; flavodoxin; 1.  
 DR Pfam; PF00175; NAD binding; 1.  
 DR PRINTS; PR00369; FLAVODOXIN.  
 DR PRINTS; PR00371; FENCR.  
 FT NON TER 1  
 SQ SEQUENCE 656 AA; 72950 MW; E73E3BD3DA8485F5 CRC64;

Query Match 13.0%; Score 710; DB 10; Length 656;  
 Best Local Similarity 29.5%; Pred. No. 3.7e-36;  
 Matches 197; Conservative 109; Mismatches 264; Indels 98; Gaps 23;

QY 448 AKSGKTPGIGSPSTEQSAKKYRKAEVNAHT--TPLLVLVYGSNMGTASTADLADIAM 505  
 DB 18 APPKPPASFRPP-----KAVDDADDGKRKRTVTFYGTGTAEFPAKMAEAK 69  
 QY 506 SK--GFAPQVATLDSHAG-----NLPRGAVLIVTASY--NGHPDNKAKQFVMDLQAS 555  
 DB 70 ARYEKVLKTVDDDDVAAEDDEYBEKTKETPLPLATYGDGEPTDVAARFYKMFTEGK 129  
 QY 556 ADEV--KGVRYVPGCGDKMATTYQKVPFIETLAKAENIADRGENDASDDEPGTY 613  
 DB 130 EKEVWLKDFNVYAVFGLNROY--EHFNKAKEVDELLEOGGNLVPVGLDDQCIEDDF 188  
 QY 614 EEMREHMSD-----VAAVFNLDIENSEDNKSTLSLOFVDSAD 652  
 DB 189 TAMKELVPELDLDRDEDDTGAATPTTAISERVVIFDKSD-----LEEDS-- 239  
 QY 653 MPLAKMHGAS-----TNVASKELQOPGASARSTRHLELPKEA--SYOEGHGLVYPR 705  
 DB 240 WTLANGNGVADADHPCAVNAVARKELKRPASDSCIHLEFDISGTGLVETGHDVGYSE 299  
 QY 706 NYEGIVNRVTARFGLDASQOIRLEABEE-----KLAHLPLAKTVSV--BLQYVEL 755  
 DB 300 NSIETVQAEFTLIDLSPTVFSIHADAEDSPKGGGSLAP--PFPSPCTRTALRLRYADL 358  
 QY 756 QDPVTRTQDLAMAKTVCPHXYELEALL--KQAYKEOVLAKRLTMLLEKVPACEM 812  
 DB 359 LNPCKKALTALAAHSDPTAEARLRFPLASPADGEYAOQIVASQSLLEVMAPSPAKP 418  
 QY 813 KFESEFI--ALLPSIRPRYSSISSPRVDEKQASITVSVSEANSGYGE-----YKGIAS 865  
 DB 419 PLGVFPALIAPIRLOPRYSSISSPKLAPRIHTCALV-----YGPRTTERIHQVCS 471  
 QY 866 NYLAEL-----QEGDTITCFISTPQSEFTLPADPETPLIMVGPCTGVAPRPGVQARKQ 919  
 DB 472 TMMKNLTLPLEVSECSWAPIFVR--QSNFRLPADPSTPIIMIGPGTGLAPFRGFLDERLA 529  
 QY 920 LKQGGSLGEAHLVFGCRSPHEDVLYQSELENAQSEGIIT-LHTAFSRMNOQKTYOVH 978  
 DB 530 LKSGAELGSSVVFPGCRNEMDYIYEELQNLQGBALSELLVAASR--BGPTREYQHK 588  
 QY 979 MEDQKGLILLDQGAHFYICGDSQMAPAVEATLMKSYADVHQVSEADARLMLQOLEEK 1038  
 DB 589 MVDKATEIMNVISQGGIYVCGDAGKAKRDVHVLHTIVQKQSLNSKTEIVYKNLQME 648  
 QY 1039 GRYAKDVW 1046

Db 649 GRYLBDVW 656

## RESULT 15

Q9SUM3 PRELIMINARY; PRT: 711 AA.

AC Q9SUM3; 01-MAY-2000 (TREMBLER1.13, Created)

DT 01-MAY-2000 (TREMBLER1.13, Last sequence update)

DT 01-MAY-2002 (TREMBLER1.20, Last annotation update)

DE NADPH-FERRIHEMOPROTEIN reductase (ATR2) (EC 1.6.2.4).

GN FN11.60 OR AT4G30210.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

OC NCBI\_TaxID=3702;

OX

RN

RP SEQUENCE FROM N.A.

RA Meyer M., Kalicki J., Wohlmann P., Smith A., Bancroft I., Mewes H.W.,

RA Beyer K.F.X., Lemcke K., Schueller C.;

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RN

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DR EMBL; AL109796; CAB52465.1; -

DR EMBL; AL161576; CAB81014.1; -

DR EMBL; AF325101; AKK17169.1; -

DR HSSP; P00388; IAO.

DR InterPro: IPR003097; PAD binding.

DR InterPro: IPR001094; Flavodoxin-like.

DR InterPro: IPR001226; Flavodoxin.

DR InterPro: IPR001709; FPN\_Cyt\_redctse.

DR InterPro: IPR001433; Oxired\_FAD/NAD(P).

DR Pfam; PF00667; FAD binding; 1.

DR Pfam; PF00258; Flavodoxin; 1.

DR Pfam; PF00175; NAD binding; 1.

DR PRINTS; PR00369; FLAVODOXIN.

DR PRINTS; PR00371; FPNCR.

KM Oxidoreductase.

SO SEQUENCE 711 AA; 78927 MW; F0503108EB7F508F CRC64;

Query Match 13.0%; Score 709; DB 10; Length 711;

Best Local Similarity 28.4%; Pred. No. 4.9e-36;

Matches 190; Conservative 120; Mismatches 264; Indels 96; Gaps 20;

Qy 434 KETTLKPEGVVAKSKIPGLIPSTEQSAKVKKAENAHNTPLVLVYSGNMGT 493

Db 81 KRVPELPK--LVIRPREBEIDG-----RKK-----VTIFRGTGTGTA 116

Qy 494 EGTARDIADIAMSKGFAP--QVATLDSHAGN-----LPREGAVLIVTASY-NGHPPDN 543

Db 117 EGFAKALGEAKAKAYEKTRFKIVLDVYAADDEVEEKLKKEDVAFPLATYGGDEPTDN 176

Qy 544 AKQFVMDLDQMS--ADSVKGVRYSVFGGDKMATTYQKVPAFIDETLAAGAENIADRG 601

Db 177 AARFYKWFTEGNDGEWLKIKYGVFGIGNROY-EHFNKAVKVVDDILVEQAGRLVQVG 235

Qy 602 EADASDDEGTVEEEMREHMSDV-----AAVENDLIDNSPDNSTL 642

Db 236 LGDDDCIEDDEFTAMREALMPELDTILREBGDAVAATPYAAVLEVVSIHSDAKFN- 294

Qy 643 SLOFVDSAAADMPILAKHNG-----AFSTNVVASKELQPGSARSIRHIEILPKKA-S 693

Db 295 -----DINNANGVTVPDAQHPRKANVAKRELHPESRSCIHLEFDIAGSGLT 345

Qy 694 YQEGDHLGVIPIRYVEGIVNVTARFGUDASQOIRLEAEERKLAHLPLAKTVSV----- 746

Db 346 YETGDHVGVLCDNLSEVDALNLDMSPTQYSLHAKED--CTPISSSLPPFPFPCNL 403

Qy 747 -EELLQVELQDPVTRTQIAMAATVCPHXYELEALL- -KOAYKEOVLAKRLTME 802

Db 404 RIALTRYACLLSPKKSALVALAAHSDPTEAERLKLHAPAGDEYSKMWVESQSLLE 463

Qy 803 LLEKYPACEMKFSFELA-LPSTRPRYYSISSGRVDEKASITVSYSGEAMSGYEYK 861

Db 464 VMAEFPSAKPPLGVFFAGVAPRLQPRFYSISSPKIAETRIHVTCALVYEMPTG-RHK 522

Qy 862 GIASNYLAELQEGDITICFISTP---QSEFTLPKQDETPLIMVPGTGVAPFRGFVQAR 917

Db 523 GVCSYMKNAVPRYKSNCSAPLFRQSNFKLPDSKVPIMIGPTGLAPFRGFIQER 582

Qy 918 KOLKEQOSLEAHLYPEGRSPHEDVLYOELEN-AQSEGITLHTAFSRMPNQKTYVQ 976

Db 583 LALVESGVLEGPVLPFGCERNRRDIFYEELQRFVESGALAEISVAFSR-EGPTKEYVQ 641

Qy 977 HWNEQDKKILIELLDQAHFYICGDSQMAPAYEATLTKSYADVDHQVSEADARMLQOLE 1036

Db 642 HKWMDKASDIWNNISQAYLYVCGDAXGMARDVHRSHTTAQEGSMDSITVABGFVNLQ 701

Qy 1037 EKGRYAKDVW 1046

Db 702 TSGRYLRDVW 711

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